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(54) Title: A NOVEL TUMOR MARKER AND NOVEL METHOD OF ISOLATING SAME		
(57) Abstract The invention encompasses a novel tumor marker which is present on tumor cells and absent on corresponding normal cells, nucleic acid encoding the tumor marker, and a novel method of isolating DNA encoding the tumor marker or a gene which is differentially expressed in tissues.		

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5 A NOVEL TUMOR MARKER AND NOVEL METHOD OF ISOLATING SAME

FIELD OF THE INVENTION

 This invention relates to proteins that serve as tumor markers for human carcinoma and to methods of isolating differentially expressed genes.

10 GOVERNMENT RIGHTS

 This invention was made in part with U.S. Government support. Therefore, the U.S. Government has certain rights in the invention.

BACKGROUND OF THE INVENTION

15 Tumor markers for human tumor cells have been largely limited to activated oncogenes and their products, for example, the myc, ras, fos, and erbB2 genes and their encoded oncoproteins. In addition, activated anti-oncogenes, such as RB, p53, and DCC, have been identified in normal cells but
20 do not appear to be present in tumor cells. Oncogene and anti-oncogene products have proven difficult to use as consistent predictors of tumor and normal tissue, respectively, due to the relatively low level of expression of the genes encoding these proteins. Thus, there is a need
25 in the art for a tumor marker which is not only differentially expressed in tumor and normal tissue, but also consistently detectable in human tumor tissue and consistently absent in the corresponding normal tissue.

 A common method used to identify genes differentially
30 or uniquely expressed in tumors, in cells responding to growth factors, and in differentiated cell types such as, among others, T cells, adipocytes, neurons, and hepatocytes is the subtractive hybridization technique (S.W. Lee et al., Proc. Natl. Acad. Sci. USA 80:4699, 1983). A method of
35 differential display of eukaryotic mRNA by means of the polymerase chain reaction (PCR) has recently been developed (P. Liang et al., Science 257:967, 1992). This method

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utilizes oligo dT linked to two additional bases as the primer for reverse transcription driven by reverse transcriptase. cDNA fragments are then amplified by Taq DNA polymerase-based PCR using an oligo dT primer along with one additional primer. The amplified cDNAs are then resolved by DNA sequencing gels. There is a need in the art for a streamlined and simplified process for isolating cDNAs corresponding to differentially expressed mRNAs.

SUMMARY OF THE INVENTION

The invention is based on the discovery of a novel protein, TC1 (SEQ ID NO:4), which is a tumor marker, particularly for invasive and metastatic tumors, and the gene encoding this protein.

The invention thus encompasses the TC1 protein (SEQ ID NO:4), which is useful as a tumor marker for tumor diagnosis and therapy, particularly for colorectal, breast, and gastrointestinal tumors, and for metastatic tumors emanating from these tumor types. TC1 is also a useful marker in general for tumor cell invasion and metastasis. mRNA encoding TC1 is not expressed in most cultured tumor cells, i.e., *in vitro*, but is expressed once these cells are grown *in vivo*. Because later stage and deeply invasive tumors contain higher levels of TC1 protein than other tumor tissues, TC1 appears to be a particularly useful marker for later stage cancers.

TC1 protein may also serve as a target in tumor targeted therapy to prevent tumor cell metastasis and thus invasion of additional organs. For example, a polypeptide fragment of the TC1 protein may be used as an antagonist of TC1 biological activity; e.g., where TC1 biological activity includes invasion and metastasis, the polypeptide fragment may be administered to a patient afflicted with the tumor in order to inhibit the spread of the tumor to other tissues. Alternatively, a truncated portion of TC1 which retains the invasive and metastatic biological activities of the full-

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length molecule will be useful for screening for antagonists of TC1 activity. Potentially useful polypeptides are described herein.

5 The invention also encompasses nucleotide probes based on the TC1 nucleotide sequence; e.g., 10, 20, 30, 40, etc. nucleotides in length. Such probes are useful for PCR-based tumor detection and *in situ* hybridization of tumor tissue sections. In addition, probes whose nucleotide sequences are based on homologies with other genes or proteins having
10 sequences related to TC1, i.e., genes of the TC1 family, two of which are described herein, are useful for detecting additional genes belonging to the TC1 family of genes.

The invention thus also encompasses methods of screening for agents which inhibit expression of the TC1 gene (SEQ ID
15 NO:3)

in vitro, comprising exposing a metastatic cell line in which TC1 mRNA is detectable in cultured cells to an agent suspected of inhibiting production of the TC1 mRNA; and determining the level of TC1 mRNA in the exposed cell line,
20 wherein a decrease in the level of TC1 mRNA after exposure of the cell line to the agent is indicative of inhibition of TC1 mRNA production.

Alternatively, the screening method may include *in vitro* screening of a metastatic cell line in which TC1 protein is
25 detectable in cultured cells to an agent suspected of inhibiting production of the TC1 protein; and determining the level of TC1 protein in the cell line, wherein a decrease in the level of TC1 protein after exposure of the cell line to the agent is indicative of inhibition of TC1 protein
30 production.

The invention also encompasses *in vivo* methods of screening for agents which inhibit expression of the TC1 gene, comprising

35 exposing a mammal having tumor cells in which TC1 mRNA or protein is detectable to an agent suspected of inhibiting production of TC1 mRNA or protein; and determining the level

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of TC1 mRNA or protein in tumor cells of the exposed mammal. A decrease in the level of TC1 mRNA or protein after exposure of the mammal to the agent is indicative of inhibition of TC1 gene expression.

5 These screening methods are particularly applicable to breast tumor cells, colon tumor cells, or tumor cells of the gastrointestinal tract.

10 The invention also encompasses a pharmaceutical composition for use in treating a late stage cancer, comprising an effective amount of an inhibitor of TC1, and a method of treating late stage cancer, comprising administering to a mammal afflicted with a late stage cancer a therapeutically effective amount of an inhibitor of TC1. Late stage cancers include those which have become deeply
15 invasive in a tissue or which have metastasized to other tissues.

20 TC1 is detectable in patient blood, urine, sputum or other body fluid using a monoclonal antibody specific for a TC1 epitope. Thus, the invention also encompasses antibodies specific for TC1, which can easily be prepared in a kit form. Monoclonal antibodies specific for TC1 may be used for tumor imaging to localize tumor position and size. TC1-specific monoclonal antibodies are also useful as screening and diagnostic agents in immunohistochemical staining of tissue
25 sections to distinguish tumor cells from normal cells. Thus, anti-TC1 antibodies are particularly useful where they recognize cells which produce the TC1 protein when such cells are paraffin-embedded and/or formalin-fixed. One example of such an antibody is the monoclonal antibody anti-TC1-1 produced by the hybridoma deposited with the American Type
30 Culture Collection as ATCC Deposit No. HB 11481.

35 In another aspect, the invention also features a novel method, called palindromic PCR, for identifying and isolating a gene, e.g., a gene which is differentially expressed in different types of tissues. The method is based on the use

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of short DNA primers and corresponding palindromic nucleotide sequences in the nucleotide sequence to be isolated.

Thus, the invention encompasses a method for producing a double stranded cDNA that includes the steps of contacting an mRNA with a DNA primer under stringent hybridization conditions to form a first hybrid molecule, the primer having a length of from 8 to 12 nucleotides and, preferably, 9 to 11 nucleotides; subjecting the first hybrid molecule to an enzyme having reverse transcriptase activity, to produce a first DNA strand complementary to at least a portion of the mRNA; contacting the first DNA strand with the primer under stringent hybridization conditions to form a second hybrid molecule; and subjecting the second hybrid molecule to an enzyme having DNA polymerase activity, to produce a second DNA strand complementary to the first DNA strand. Preferably, the method also includes the step of amplifying the first and second DNA strands.

In preferred embodiments, a single enzyme provides both the reverse transcriptase activity and the DNA polymerase activity. One example of a suitable such enzyme is rTth DNA polymerase from the thermophilic eubacterium *Thermus thermophilus*.

As used herein, the term "palindromic nucleotide sequences" means that a double stranded DNA molecule contains a specific DNA sequence in both its coding strand and its anti-parallel strand, when those strands are read in the same direction, e.g., 5' to 3'.

The specific sequence of the DNA primer is arbitrary in that it is based upon individual judgment. In some instances, the sequence can be entirely random or partly random for one or more bases. Preferably, the GC content of the primer is between 40% and 60%, most preferably about 50%. In other instances, the arbitrary sequence can be selected to contain a specific ratio of each deoxynucleotide. The arbitrary sequence can also be selected to contain, or not

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to contain, a recognition site for a specific restriction endonuclease.

The DNA primer can contain a sequence that is known to be a "consensus sequence" of an mRNA of known sequence. As defined herein, a "consensus sequence" is a sequence that has been found in a gene family of proteins having a similar function or similar properties. The use of a primer that includes a consensus sequence may result in the cloning of additional members of a desired gene family.

Palindromic PCR enables genes that are altered in their frequency of expression, as well as those that are constitutively or differentially expressed, to be identified by simple visual inspection and isolated. The method also allows the cloning and sequencing of selected mRNAs, so that the investigator may determine the relative desirability of the gene product prior to screening a comprehensive cDNA library for the full length gene product.

Further objects and advantages of the invention will be apparent in light of the following description and the claims.

BRIEF DESCRIPTION OF THE DRAWINGS

Fig. 1 is a polyacrylamide gel of size-separated cDNAs that were reverse transcribed from paired mRNAs from colon carcinoma (T) and adjacent normal colon tissue (N) and subsequently amplified.

Fig. 2A is a gel in which the TC1 cDNA fragment identified in Fig. 1 was recovered and re-amplified.

Fig. 2B is a Northern Blot of three pairs of RNA from colon carcinoma (T) and their adjacent normal colon tissue (N) probed with 32P-labeled TC1 cDNA.

Fig. 3 shows the nucleotide sequence (described herein as SEQ ID NO:1) and corresponding amino acid sequence (SEQ ID NO:2) of the 636 bp partial TC1 clone.

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Fig. 4 shows the nucleotide sequence (SEQ ID NO:3) and corresponding amino acid sequence (SEQ ID NO:4) of the full-length TC1 gene and protein.

Fig. 5 is a sequence comparison of the four internal homologous domains of TC1 (SEQ ID NO:4), each approximately 135 amino acids.

Fig. 6A is a schematic representation of the four repeats of TC1.

Fig. 6B is a proposed schematic arrangement of the four repeated domains and the N- and C-terminal domains.

Fig. 7 shows the amino acid sequence identity between TC1 (SEQ ID NO:4) and Big-h3 (SEQ ID NO:17).

Fig. 8 is a Northern Blot of five pairs of RNA from colon carcinoma (T) and adjacent normal colon tissue (N) probed with 32P-labeled Big-h3 cDNA, the bottom panel representing control RNA probed with 32P-labeled B-actin.

Fig. 9 shows amino acid sequence homology between TC1 (SEQ ID NO:4) and Fasciclin I from Grasshopper (GrF) (SEQ ID NO:18) and Drosophila (DrF) (SEQ ID NO:19).

Fig. 10 is a Schematic representation showing that, on average, in every 202 bases of sequence in one strand of cDNA, there is one 9-base sequence exactly palindromic to that in a region of its antiparallel strand.

Fig. 11 shows the relationship between the palindromic frequency and the number of bases in a putative DNA primer, as determined by cDNA Matrix analysis.

Fig. 12 is a schematic representation of the method of the invention, palindromic PCR, driven by the enzyme rTth DNA polymerase with one DNA primer in one reaction tube; the dotted line indicates mRNA and the solid line indicates cDNA; the short jagged line represents the single DNA primer.

Fig. 13A shows the effect of the length of the DNA primer on the cDNA amplification patterns; the length and nucleotide sequence of each primer are: A, 8-mer (5'-TGTCGAGA); B', 9-mer (5'-TGTCAGAC); C', 10-mer (5'-

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TGTCCAGATG) (SEQ ID NO:5); D', 11-mer (5'-TGTCCAGATGC) (SEQ ID NO:6); E', 12-mer (5'-TGTCCAGATGAC) (SEQ ID NO:7).

Fig. 13B shows the effect of the GC content of the DNA primer on the cDNA amplification patterns; the GC content and nucleotide sequence of each primer (10-mer) are: A', 40% (5'-TGTCCAGATA) (SEQ ID NO:8); B', 50% (5'-TGTCCAGATG) (SEQ ID NO:5); C', 60% (5'-TGTCCAGACG) (SEQ ID NO:9); D', 70% (5'-TGTCCAGCCG) (SEQ ID NO:10); E', 80% (5'-TGTCGCGCCG) (SEQ ID NO:11); F', 90% (5'-TGCCGCGCCG) (SEQ ID NO:12).

Fig. 13C shows the effect of the sequence specificity of the DNA primer on the cDNA amplification patterns; 10-mer primers with the same GC content but different sequences are: A', 5'-TGATGCACTC (SEQ ID NO:13); B', 5'-TGAGCTACTC (SEQ ID NO:14); C', 5'-TGACTGACTC (SEQ ID NO:15).

Fig. 13D shows palindromic PCR performed by rTth DNA polymerase (A) with reverse transcription cycles (RT cycles) and (B) without RT cycles.

Fig. 14 shows the identification of differentially expressed genes in human colon carcinoma.

Fig. 15 shows reamplification of the TC1 cDNA fragment isolated from colon carcinoma; the PCR product was analyzed on a 1.0% agarose gel; a 0.63 Kb cDNA fragment (arrow) was detected.

Fig. 16 is an autoradiogram of DNA sequencing gels showing the presence of PP1 primer sequence (5'-CTGATCCATG) (SEQ ID NO:16) at the 5'-end of both strands of the TC1 cDNA fragment; cloning sites are indicated by arrows, sequences below arrows are pBS (KS) vector sequences reading from T3 primer and T7 primer.

Fig. 17 is a Northern Blot of 24 pairs of colon carcinoma (T) and their adjacent normal tissue (N) probed with ³²P-labeled TC1 cDNA.

Fig. 18 shows the Tumor/Normal RNA Ratio from Northern Blot results of Fig. 17.

Fig. 19 is a Northern Blot of RNA from carcinoma cells which result from metastasis from colon carcinoma to liver

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(LM) and their adjacent normal liver (NL) probed with ³²P-labeled TC1 cDNA.

Fig. 20 shows a Northern Blot of RNA from breast cancer cell line MCF-7 (1) and colon cancer cell line CX-1 (2) cultured *in vitro*, and MCF-7 tumor (3) and CX-1 tumor (4) grown *in vivo* in nude mice.

Fig. 21 shows staining of formalin-fixed and paraffin-embedded colon tumor tissue sections using the monoclonal antibody anti-TC1-1 and avidin-biotin-peroxidase detection.

Fig. 22 shows staining as described in Fig. 21, except that panels A, C, D represent breast invasive ductal carcinoma and panel B, normal breast tissue.

Fig. 23 shows staining as in Fig. 13, except that panels A and B represent gastric carcinoma, and panels C and D, deeply invasive colon carcinoma.

Fig. 24 is a Western Blot analysis of protein samples from two pairs of colon carcinoma and their adjacent normal colon (A) and two pairs of breast carcinoma and their adjacent normal breast (B), using a monoclonal antibody against TC1 protein as a probe.

Fig. 25A shows the ethidium bromide staining pattern of an RNA gel in which the same amount of RNA from JMN (1) and JMN1B (2) cells is loaded per lane.

Fig. 25B is a Northern Blot analysis of RNA from malignant mesothelioma cells JMN1B (2) and JMN (1) using TC1 cDNA as a probe.

Fig. 26 is a Western blot using a monoclonal antibody against TC1 to probe JMN1B cells grown in conditioned medium and whole cell lysate.

Fig. 27 shows JMN1B cells fixed with paraformaldehyde without subsequent permeabilization in panels A and B, and JMN1B cells fixed with paraformaldehyde and then permeabilized in panels C and D.

Figs. 28A-28D show the corrected nucleotide sequence and corresponding amino acid sequence of the full length TC1 gene and protein.

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DESCRIPTION OF THE PREFERRED EMBODIMENTS

TC1 (SEQ ID NO:4) is a novel protein that is found in invasive and metastatic tumor cells. The nucleotide sequence (SEQ ID NO:3) encoding TC1 was found using a novel technique described herein as palindromic PCR, a technique which enables identification and cloning of a gene that is differentially expressed in tissues. Cloning and sequencing of the gene encoding TC1 and characterization of the protein is described below, along with examples of how the protein is detected in invasive and metastatic cancers. Examples describing additional uses of the TC1 protein and its fragments, the nucleotide sequence encoding TC1 and fragments thereof, and antibodies specific for TC1 are also included.

Identification, Cloning and Detection of Expression of the TC1 Gene

The identification, cloning, and differential detection of expression of the TC1 gene (SEQ ID NO:3) was performed as follows. A 636 bp cDNA fragment (SEQ ID NO:1) containing TC1 sequences was identified and isolated by a rapid method termed palindromic PCR, described herein, from human surgical colon carcinoma tissue. Briefly, paired mRNAs were isolated from colon carcinoma tissue and adjacent normal colon tissue from the same patient, then matched mRNAs were reverse transcribed to cDNA and subsequently amplified by the palindromic PCR method described herein, which utilizes one DNA primer. Both reverse transcription and PCR reactions were driven by a single enzyme, rTth DNA polymerase, in a single tube. ³⁵S or ³³P-labeled PCR cDNA fragments were resolved on a DNA sequencing gel. As shown in Fig. 1, paired mRNAs from colon carcinoma (T) and adjacent normal colon tissue (N) were reverse transcribed to cDNA and subsequently amplified by palindromic PCR. ³⁵S-labeled PCR cDNA fragments were then resolved on a DNA sequencing gel. A differential cDNA band (TC1) appeared to be present only in the tumor sample. This TC1 cDNA fragment was recovered from the

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sequencing gel and then reamplified with the same palindromic primer. This 636 bp fragment is identified with a horizontal arrow in Fig. 2A.

5 TC1 gene expression was examined in colon carcinoma cells and in the corresponding adjacent colon tissue, and the results were as follows. Fig. 2B is a Northern Blot of three pairs of RNA from colon carcinoma (T) and their adjacent normal colon tissue (N) probed with ³²P-labeled TC1 cDNA. TC1 mRNA was over-expressed in all three cases of colon carcinoma, whereas only very weak TC1 message appeared in the adjacent normal tissue. In the bottom panel of the blot, control RNA was blotted with ³²P-labeled cDNA encoding B-actin.

10 Northern Blot analysis of several pairs of Tumor/Normal total RNA using a ³²P-labeled TC1 cDNA probe revealed that the TC1 mRNA size is about 3.6Kb. This first TC1 cDNA fragment was cloned into a pBluescript plasmid DNA vector strategies. Nucleotide sequence analysis revealed that this fragment contained 636bp with nucleotide sequences corresponding to the primer sequence at both 5'-ends of the double-stranded DNA (Fig. 3 and SEQ ID NO: 1). The corresponding predicted amino acid sequence is shown in Fig. 3 and provided in SEQ ID NO: 2. A search of the GenBank database with this cDNA fragment revealed that TC1 is a novel gene.

25 Nucleotide sequence analysis of the 636bp TC1 cDNA fragment obtained by the described differential display method revealed that it contained a partial open reading frame. Therefore, this 636bp cDNA fragment was used as probe to screen a cDNA library. Several overlapping clones were obtained and contained a 2997bp sequence. To obtain the complete open reading frame for TC1, a modified 5'-end RACE technique was used to amplify the TC1 coding regions. The nucleotide and deduced amino acid sequence of full-length TC1 is shown in Fig. 4 and provided in SEQ ID NOS: 3 and 4. The N-terminal signal sequence is underlined; one predicted N-linked glycosylation site (NDT) is boxed and a

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polyadenylation signal (AATAAA) is indicated. The cDNA contains 3126bp with a potential polyadenylation sequences (AATAAA) at the 3'-end, beginning at residue 2963. The open reading frame (ORF) encodes a 777-amino acid protein with a calculated molecular weight of 86kD. The TC1 protein contains an amino-terminal signal peptide or secretory leader signal (ALPARIILALALALAL), and one predicted site of N-linked glycosylation at amino acid residue 605 (NDT). One Cemokine B family motif (C-C) was found at amino acid residue 85 (C-C) of TC1.

Analysis of the deduced amino acid sequence (SEQ ID NO:4) revealed that TC1 contained four internal homologous domains of approximately 135 amino acids. A comparison of these repeats is shown in Fig. 5. Each boxed amino acid is identical with at least one other residue at that same position. The interdomain homologies range from 32% (between domains 2 and 4) to 18% (between domains 1 and 3). Some amino acid sequence such as TLF $\frac{A}{V}$ P $\frac{T}{S}$ NEAF, NGVIHXID are highly

conserved between all four repeats. The notations $\frac{A}{V}$ and $\frac{T}{S}$

are used herein to indicate that alanine or valine, and threonine or serine, respectively, may be found at these positions. In addition, the notation X is used herein to indicate that this position may include any amino acid. Each repeat starts with the most divergent sequence. The four repeats occur between residues 139-537 and are uninterrupted by non-homologous domains. A schematic representation of the four repeats of TC1 is shown in Fig. 6A. The four homologous repeats suggest a tetrameric structure (Mclachlan 1980; Zinn et al, 1988) with two binding sites, one at each intrachain dimer. The four repeats of TC1 may serve as ligand binding sites, with the N-terminal or C-terminal domains serving as the functional domain. One possible arrangement of the four repeated domains and the N- and C-terminal domains is shown schematically in Fig. 6B.

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The nucleotide and corresponding amino acid sequence of the TC1 gene and protein with a corrected leader signal sequence are given in Figs. 28A-28D.

Palindromic PCR

5 Described below is a novel technique used to identify the TC1 mRNA and prepare TC1 cDNA. Although the sequence of bases in a coding and antisense strand of a cDNA molecule are, in a sense, "mirror images" of one another, we have found that with surprising frequency a short sequence of
10 bases, e.g. 9 or 10, in one strand will be found to have an exact copy in its anti-parallel strand. We call these sequences "palindromic" sequences. This phenomenon has been used to develop a method of cDNA isolation and amplification.

15 In order to determine the frequency of occurrence or "palindromic frequency" of these anti-parallel repeats, a computer program called DNA Matrix (DNA Strider 1.2) was used to analyze double stranded cDNAs which were randomly selected from the GenBank database. DNA matrix analysis revealed the palindromic frequency of double strand cDNA to be
20 surprisingly high and led to our development of a relationship between the number of bases in the chosen sequence, the "palindromic bases," and the palindromic frequency. Single strand cDNA (the mRNA strand) and its anti-parallel strand were compared, each from the 5' to 3' end by the DNA Matrix program. For example, as illustrated
25 in Fig. 10, on the average, in every 202 bases of sequence in one strand of cDNA, there is one 9-base sequence that is exactly duplicated to that in another region of its antiparallel strand. The palindromic frequency found in
30 native cDNA is much higher than that which would be calculated from random composition, suggesting that the nucleotide composition of double-stranded cDNA follows certain palindromic rules. As shown in Fig. 11, the palindromic frequency dramatically decreases when the number
35 of bases in the searched segment increases. The key numbers

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of bases which lead to dramatic change of palindromic frequency are 9, 10 and 11 bases. This, then, is the theoretical basis for designing a primer for use in the DNA isolation and amplification method of the invention, palindromic PCR.

Table 1 presents the statistical data showing the palindromic frequency related to the number of bases in the searched segment.

Table 1
Palindromic Frequency Related to
No. of Bases in Searched Segment as
Revealed by cDNA Matrix
Analysis

No. Bases in Searched Segment (X Bases)	Average Length to Find One X-Base Palindromic Sequence	Palindromic Frequency
7 bases	18 bases	0.4
9 bases	202 bases	0.048
11 bases	872 bases	0.015
13 bases	>1996 bases	<0.007

The principle of the method of palindromic PCR is shown in schematic representation in Fig. 12. The general strategy is to use a single primer and one enzyme combining both reverse transcriptase and DNA polymerase activities, e.g., rTth DNA polymerase (from the thermophilic eubacterium *Thermus thermophilus*), to perform both reverse transcription and polymerase chain reaction in one reaction tube. rTth DNA polymerase possesses a very efficient reverse transcriptase activity in the presence of $MnCl_2$ and a thermostable DNA polymerase activity in the presence of $MgCl_2$. The rTth DNA polymerase has been observed to be greater than 100-fold more efficient in coupled reverse transcription and PCR than the analogous DNA polymerase, Taq (T. W. Myers et al., *Biochemistry* 30:7661, 1991). In this reaction, an appropriate primer would allow anchored annealing to some regions of certain mRNA species that contain sequence complementary to the palindromic primer. This subpopulation

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of mRNAs is likely to be reverse transcribed by rTth DNA polymerase. A "Palindromic" primer apparently has a greater probability of anchoring to the coding regions of mRNA than oligodT primer. Once mRNAs are reverse transcribed to form a first strand cDNA species, the same primer can anneal to some regions of the first strand cDNA and function as the "Downstream primer" in a PCR reaction. The same primer can also function as the "Upstream primer." When the primer anchors to first strand cDNAs, the annealing position to various cDNA molecules should, in principle, be at different distances in different molecules from the first annealing position. Therefore, the amplified cDNA fragments from various mRNAs will be of different sizes. Once these PCR-generated cDNA fragments are labeled with ³⁵S-dATP or ³³P-dATP, they can be resolved as a ladder by DNA sequencing gels. A display of cDNAs originating from various mRNAs can then be visualized after autoradiography.

The selection of the specific palindromic primer depends on three important factors: the length, the GC content, and the sequence specificity. DNA Matrix analysis has indicated that the ideal length of a primer for an appropriate palindromic frequency is from 9 to 11 bases. Therefore, a set of primers from 8 base to 12 base in length with 50% GC content was chosen for study. Our results showed that 9, 10, and 11 base primers gave an appropriate number of cDNA fragments readily resolvable by DNA sequencing gels (Fig. 13). To identify the GC content of the primer most suitable for this method, a set of 10-mer primers with GC content ranging from 40% to 90% was tested. The results suggested that a GC content from 40% to 80% is acceptable (Fig. 13). However, primers with 40% to 60% GC content appear to yield better results. To examine the effect of the specific sequence of the primer, 10-mer primers of different sequences each having 50% GC content was tested. As predicted, different primers gave rise to different cDNA

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patterns (Fig. 13). As little a difference as three bases led to totally different cDNA profiles.

cDNA patterns generated by palindromic PCR are highly stable. When the same conditions were used but the experiments repeated at different times, the patterns of the amplified cDNA fragments were highly reproduced, indicating the reliability of this method.

In order to be sure of detecting mRNAs with a low copy number, it was necessary to determine the sensitivity of this method. It has been reported that the amplification driven by rTth DNA polymerase is at least 100-fold greater than that by Taq polymerase. rTth DNA polymerase allows the detection of IL-1a mRNA, which has a very low copy number, in 80pg of total cellular RNA (T.W. Myers et al., Biochemistry 30:7661, 1991). Thus, the higher efficiency of rTth DNA polymerase ensures that the palindromic PCR method of the invention provides high sensitivity. In addition, because rTth polymerase is thermostable, it can also be used to perform several RT cycles (reverse transcription cycles), which means several copies of first strand cDNA can be obtained from a single copy of mRNA. The sensitivity of the method is increased by performing multiple RT cycles using rTth polymerase (Fig. 13).

The method of the invention was tested in a search for differences in mRNA expression between human colon carcinoma and the adjacent normal epithelium from a surgical specimen. Paired mRNA preparations were reverse transcribed with a palindromic primer 5'-CTGATCCATG (designated as PP-1 primer) (SEQ ID NO:16) in the presence of MnCl₂, followed by PCR with the same primer in the presence of MgCl₂, using rTth DNA polymerase. The reaction products were then analyzed by DNA sequencing gels. About 70-110 amplified cDNA fragments ranging from 100-700 bases from both preparations were detected (Fig. 14). Whereas overall cDNA patterns between tumor and normal tissue are similar, significant differences were detected by this method. Most cDNA bands showed the

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same intensity between tumor and normal preparations, but two cDNA bands designated as TC1 and TC2 appeared with increased intensities in tumor tissue (Fig. 14). A sample reaction protocol is described below.

5 To 1.1 μ l of double distilled (dd) H₂O is added 0.5 μ l of 10X rTth DNA polymerase reverse transcriptase (RT) buffer (100mM Tris-HCl, pH 8.3, 900mM KCl), 0.5 μ l of 10mM MnCl₂, 0.4 μ l of 2.50mM dNTP, 1.0 μ l (0.50 μ g) of one palindromic primer (9-11 mer), and 1.0 μ l (100 ng) of mRNA to form Mix A in a total vol. of 4.5 μ l. Mix A is heated in a 0.5 ml PCR tube at 65°C for 6 min and then at 37°C for 8 min. Next, 0.5 μ l (1.25 unit) of rTth DNA polymerase is added, the reaction mixture is mixed well, spun briefly, incubated at 70°C for 12 min and then placed on ice. Mix B which consisting of 15 12.5 μ l of dd H₂O, 2.0 μ l of 10X chelating buffer (50% glycerol (v/v), 100mM Tris-HCl, pH 8.3, 1M KCl, 0.5% Tween 20), 2.0 μ l of 25 mM MgCl₂ solution, 2.50 mM dNTP and 2.0 μ l of ³⁵S-dATP (or ³³P-dATP) is dispensed in the amount of 20 μ l into each 5.0 μ l RT reaction mixture. The samples are mixed and spun briefly and then overlaid with 25 μ l of mineral oil. 20 The polymerase chain reaction is then started: 94°C for 40 sec., 40°C for 2 min., 72°C for 35 sec. (for 40 cycles, hold at 72°C for 4 min.), and then 4°C.

25 For cDNA analysis, 7 μ l of a PCR sample is mixed with 4 μ l of sequencing loading buffer, samples are incubated at 80°C for 3 min., and then placed on ice. 4.5 μ l of the sample is loaded on a 6%-8% agarose DNA sequencing gel.

30 A gel slice containing a desirable cDNA band (such as TC1) was soaked in 200 μ l of ddH₂O for 20 min and then separated from 3M paper with a clean forcep or a plastic pipette tip. The gel was removed and pounded with an autoclaved plastic pipette tip. Elution buffer (20 μ l) was added and the mixture was vortexed and left at room temperature for 4 hrs or overnight. After centrifugation, 35 cDNA fragments in 10 μ l eluent were reamplified by rTth DNA polymerase with the same palindromic primer, as described.

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After one 40-cycle PCR, the reamplified cDNA could be detected by agrose gels stained with ethidium bromide. The amount of cDNA generated was sufficient for cloning and preparing a probe for Northern Blot analysis. Fig. 15 shows the gel obtained when the TC1 cDNA band was subjected to elution and reamplification. Total PCR product of the TC1 fragment was 2.5 μ g.

The reamplified TC1 cDNA fragment was treated with T4 DNA polymerase and cloned into pBluescript plasmid DNA vector at SmaI site by blunt end ligation. The nucleotide sequence of the TC1 fragment (SEQ ID NO:1) showed that a sequence identical to the PP1 primer (SEQ ID NO:16) is indeed present at the 5'-end of both strands of the TC1 fragment (Fig. 16). This result confirms that the 5'-ends of both complementary chains of the TC1 cDNA fragment used the same palindromic primer during palindromic PCR as discussed above. It also implies that the same palindromic primer sequence is present at the 5'-ends of both strands for every PCR product in the same reaction. These results establish that a single 9-11 base palindromic primer can effectively prime reverse transcription and then serve as both a "Downstream primer" and an "Upstream primer" in palindromic PCR amplification.

The method of the invention differs from other methods in a number of ways. In palindromic PCR, only a single primer (9-11 bases) is used and is sufficient to prime reverse transcription as well as to support subsequent PCR for a display of nearly 100 cDNA species. Because the pattern of amplified cDNAs depends on the sequence of the single palindromic primer, the species of mRNAs that are subjected to amplification can readily be controlled by a proper sequence of the palindromic primer. If a group or family of genes shares certain sequences, a primer can be chosen from such a sequence, and a specific display of this set of mRNAs can readily be performed. Likewise, computer analysis of the Genbank database may reveal additional sequences useful as a primer shared by a set of related

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genes. The use of such a primer by the method of the invention would allow the display for the expression of a given set of genes. Palindromic PCR provides an easy, sensitive and economical way to identify and isolate differentially expressed genes related to tumor and other disease.

Differential expression of TC1 DNA in normal tissue and tumor cells.

Northern Blot analysis, as described above, confirmed the differential expression of TC1 mRNA in colon carcinoma tissue, and the absence of TC1 mRNA in the corresponding normal tissue. Evaluation of the expression of TC1 mRNA in additional cases of colon carcinoma at different stages was also undertaken. Surgical specimens of 24 cases of human primary colon carcinoma and 6 cases of liver metastases were examined by Northern hybridization of total RNA with ³²P-labeled TC1 probe.

A Northern Blot of 24 pairs of colon carcinoma (T) and their adjacent normal tissue (N) probed with ³²P-labeled TC1 cDNA is shown in Fig. 17. It is evident from the results that the level of TC1 mRNA in tumor tissue is much greater than the level in adjacent normal tissue in all 24 cases. The TC1 mRNA levels vary in different cases of carcinoma. Panels I and II show A: TC1 mRNA and B: Control; Panel III shows TC1 mRNA and control (Actin) mRNA.

Fig. 18 shows the Tumor/Normal RNA Ratio from Northern Blot results of Fig. 17. The horizontal line indicates the mean Tumor/Normal ratio. TC1 mRNA was abundantly expressed in all 24 cases of primary colon carcinoma and 6 cases of liver metastases, whereas only a small amount of TC1 mRNA was detected in a few cases of paired adjacent normal tissue. The mRNA level of TC1 was much greater in primary colon carcinoma than in paired adjacent normal colonic epithelium in all 24 cases. The Tumor/Normal ratio varied from 5.6 to 92, and the mean Tumor/Normal ratio being 32. The Tumor/Normal ratio, when plotted against the Duke's stage of

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disease, gave evidence for increasing TC1 expression with increasing stage of colon carcinoma.

In all six cases of paired colon carcinoma metastatic to liver, the TC1 mRNA level was much higher in metastatic tumor than in adjacent normal liver tissue. Fig. 19 shows a Northern Blot of RNA from metastatic colon carcinoma to liver (LM) and their adjacent normal liver (NL) probed with ³²P-labeled TC1 cDNA. TC1 mRNA was expressed only in metastatic tumor in 5 of 6 samples. Only one sample of normal liver tissue expressed a very weak TC1 message. The Tumor/Normal ratio is greater than 64. These results suggested that differential expression of TC1 may be associated with human colorectal cancer progression and biological aggressiveness of the disease.

In vivo and in vitro expression of TC1 mRNA

The expression of TC1 mRNA in cultured cancer cells and *in vivo* tumor cells was analyzed and is described below. TC1 was overexpressed in tumor tissue *in vivo*. The expression of TC1 mRNA in cultured cancer cell lines *in vitro* was examined by Northern Blot analysis. RNAs isolated from twelve colon cancer cell lines (HT29, Clone A, MIP101, CX-1, Morser, CCL227, CCL228, etc.) derived from different stage of human colon carcinoma, two melanoma cell lines (LOX, A2058), one breast cancer cell line (MCF-7), two cervical cancer cell lines (Hela, A431), three bladder cancer cell lines (EJ, T24, MB49), one pancreas cancer cell line (CRL1420), two hepatoma cell lines (HepG2, HepG3) and four normal cell lines (FS-2, MRC-5, 498A, CV-1) were screened by Northern Blot analysis. However, the TC1 transcript could not be detected in all of these cell lines. This result suggested that TC1 expression was dramatically decreased or indeed turned off in cultured cancer cells. However, after cultured cancer cells were injected into nude mice to grow tumor *in vivo*, TC1 mRNA expression turned on again and its mRNA level could be detected by Northern Blot analysis.

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Fig. 20 shows a Northern Blot of RNA from breast cancer cell line MCF-7 (1) and colon cancer cell line CX-1 (2) cultured *in vitro*, and MCF-7 tumor (3) and CX-1 tumor (4) grown *in vivo* in nude mice. TC1 mRNA in colon cancer cell line CX-1 and breast cancer cell line MCF-7 cultured *in vitro* could not be detected by Northern Blot analysis. After cultured CX-1 and HT29 cells were injected into nude mice to form tumors *in vivo*, TC1 mRNA was detectable by Northern Blot analysis, the TC1 mRNA levels being dramatically increased *in vivo*. This result suggests that TC1 gene expression was turned on or dramatically increased in the tumor cells *in vivo*. Thus, the differential expression of the TC1 gene appears to be related to invasion and metastasis of tumor cells *in vivo*. The regulation of TC1 gene expression *in vivo* and *in vitro* could be a very important model to understand tumorigenesis and tumor malignant behavior.

Expression of TC1 protein

The expression of TC1 protein in *in vivo* tumor cells, cultured carcinoma cells, and in corresponding normal cells was examined, and is described below. The TC1 gene (SEQ ID NO:3) was cloned into a plasmid expression vector, and recombinant TC1 protein (SEQ ID NO:4) was expressed in bacteria. Several monoclonal antibodies against the bacterially-produced TC1 protein were raised, as will be described below. A variety of formalin-fixed and paraffin-embedded tumor tissue sections were examined by immunohistochemical staining with a mouse monoclonal anti-TC1 antibody anti-TC1-1 using an avidin-biotinylated-peroxidase detection technique. Strong positive staining of TC1 was found in primary colon carcinoma (Fig. 21, panel A), colon carcinoma metastatic to liver (Fig. 21, panel C) and lymph node (Fig. 21, panel D), breast carcinoma (Fig. 22, panels A,C,D) and gastric carcinoma (Fig. 23, panels A,B). The TC1 protein level in tumor tissue is much greater than the level of TC1 in adjacent normal tissue (Figs. 21B, 23B).

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These results, which represent the staining of sixteen cases of different stages of primary colon carcinoma, eight cases of colon tumor metastatic to liver and lymph node, fourteen cases of breast carcinoma and five cases of gastric carcinoma, suggested the following three conclusions. First, the TC1 protein level appeared to be different in different types of carcinoma, with protein levels being highest in breast carcinoma. Second, the advance edge of the deeper invasive tumor appeared stain stronger for TC1, suggesting a greater prevalence of TC1 protein at the advance edge of the tissue. Third, the more advanced stages of tumor appeared to contain more TC1 protein.

Fig. 24 is a Western Blot analysis of protein samples from two pairs of colon carcinoma and their adjacent normal colon (A) and two pairs of breast carcinoma and their adjacent normal breast (B), using a monoclonal antibody against TC1 protein as a probe. A major 86kd protein (arrow) was detected by anti-TC1 antibody in tumor samples (T) but not in normal samples (N). The Western Blot analysis confirmed that tumor tissue contained significantly more TC1 protein than the corresponding adjacent normal tissue.

TC1 gene expression

The presence of TC1 mRNA and protein in malignant mesothelioma cells was examined, and is described below. More than 42 cell lines have been screened for TC1 gene expression by Northern Blot analysis. However, only two cell lines, JMN1B and JMN, express detectable mRNA by Northern Blot analysis. JMN1B and JMN are malignant mesothelioma, JMN1B being a subline of JMN cells with showing enhanced tumorigenicity after passage of JMN cells through a nude mouse. Fig. 25 is a Northern Blot analysis of RNA from malignant mesothelioma cells JMN1B and JMN using TC1 cDNA as a probe. The results presented in Panel 25B demonstrate that TC1 mRNA level in JMN1B cells (2) is much greater than that in JMN cells (1). Panel 25A shows the ethidium bromide

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staining pattern of an RNA gel in which the same amount of JMN (1) and JMN1B (2) RNA is loaded per lane.

5 The Northern Blot analysis revealed that the TC1 mRNA level is much higher in JMN1B than in JMN, the JMN1B/JMN ratio being approximately 14. Higher expression of TC1 mRNA in JMN1B could be related to the observed greater tumorigenicity of JMN1B cells. It has been found that JMN1B cells can secrete an "EGF-like" growth factor called transformed mesothelial growth factor (TMGF) that satisfies the EGF requirement of normal human mesothelial cells. The difference in the levels of TC1 mRNA in JMN1B and JMN cells provides an ideal cell model to understand the regulation of TC1 expression and its relation to tumorigenicity.

10 Sequence analysis of the deduced amino acid sequence has revealed that the TC1 protein (SEQ ID NO:4) contained a secretory leader signal at its N-terminus. The secretion of TC1 protein was confirmed by Western Blot analysis of conditioned medium of JMN1B cells. JMN1B cells were cultured in regular medium until 90% confluent, then cultured in serum free medium for two days. This serum free conditioned medium was analyzed by immunoblotting with anti-TC1 monoclonal antibody. Fig. 26 is a Western blot analysis using a monoclonal antibody against TC1 to probe JMN1B cells grown in conditioned medium and whole cell lysate. Two major bands (about 86kd and 104kd) were recognized by anti-TC1 antibody both in JMN1B cell conditioned medium (1) and whole cell lysate (2). Numbers on the left indicate the position of molecular weight standards in kilodalton. The protein size of the lower molecular weight 86kd band is consistent with that of deduced TC1 protein, whereas the higher molecular weight 104kd band is consistent with a TC1 glycoprotein. There is one predicted site of N-linked glycosylation at the amino acid residue 605(NDT) of deduced TC1 protein sequence. There are 60 threonine residues and 36 serine residues in the deduced TC1 sequence, each of which is a potential site of O-linked glycosylation.

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Human malignant mesothelioma cell line JMN1B can express abundant TC1. This cell line was used to study the distribution and localization of TC1 protein by immunofluorescent staining with an anti-TC1 monoclonal antibody followed by Rhodamine conjugated goat anti-mouse IgG secondary antibody. When JMN1B cells were fixed with paraformaldehyde without subsequent permeabilization, the positive staining was seen on the cell surface or outside of the cell (Fig. 27, panels A,B), which confirms the secretion of TC1 protein. When JMN1B cells were fixed with paraformaldehyde and then permeabilized, positive staining appeared in the Golgi complex and the endoplasmic reticulum (ER) in the cell (Fig. 27, panels C,D), suggesting that TC1 protein is synthesized in the ER and Golgi complex. The staining in the Golgi complex is clearly evident, indicating that glycosylation of TC1 protein may be located in the Golgi complex. The TC1 protein distribution pattern also suggests that TC1 is a secreted glycoprotein.

Without being bound to one theory as to the biological function of TC1, observations as to the prevalence and expression of TC1 mRNA and protein indicate that TC1 may be related to tumor malignant behavior such as invasion and metastases. These observations include the following: TC1 is significantly overexpressed in tumor tissue; TC1 is a secreted protein; later stage tumor expresses higher levels of TC1; deeper invasive tumor contains higher levels of TC1 protein; TC1 expression turns off in cultured tumor cells *in vitro* and turns on again after cells grow tumor tissue *in vivo*. These observations indicate that the function of TC1 is not related to tumor cell proliferation, but is more likely involved in tumor malignant behavior *in vivo*, such as invasion and metastases.

TC1 is a member of a Family of Proteins.

A FASTA search of the GenBank and EMBL database with the TC1 open reading frame indicated that the protein is unique.

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However, TC1 whole protein shared 45% sequence identity with a TGF-beta inducible gene, Big-h3, at the amino acid level, suggesting that TC1 and Big-h3 may belong to a new gene family. The identity between TC1 (SEQ ID NO:4) and Big-h3 (SEQ ID NO:11) at the amino acid level is shown in Fig. 7. In Fig. 7, identical amino acids between TC1 and Big-h3 are boxed. Several stretches of amino acids GSFTXFAPSNEAW, TLXAPTNEAFEKXP, ATNGVVHXID XV, LYXGQXLETXGGKXLRV FVYR, HYPNGXVTVN CAR are highly conserved between TC1 and Big-h3. Northern Blot analysis showed that the TC1 gene is expressed from a larger transcript than Big-h3, and DNA sequence analysis indicated that TC1 contains a longer open reading frame encoding a higher molecular weight protein than the Big-h3 gene. It has been found that Big-h3 also contains four internal repeats. The amino acid sequence homology and structural similarity between TC1 and Big-h3 indicate their functional similarity and relationship. We found that Big-h3 mRNA is also much more abundant in colon carcinoma tissue than in adjacent normal colon tissue (Fig. 7). Fig. 8 is a Northern Blot of five pairs of RNA from colon carcinoma (T) and adjacent normal colon tissue (N) probed with ³²P-labeled Big-h3 cDNA. The blot shows Big-h3 mRNA level in colon carcinoma to be much higher than that in adjacent normal tissue. The bottom panel represents control RNA probed with ³²P-labeled B-actin.

In contrast to the expression pattern of TC1 mRNA, which is shown to be largely restricted to *in vivo* tumor tissue, Big-h3 mRNA is not only expressed in the tumor tissue, but also expressed in the cultured tumor cell lines and some normal cell lines. Though TC1 and Big-h3 shared significant homology, their responses to growth factors are distinctly different.

Fasciclin I, II, III are extrinsic membrane glycoproteins involved in the growth cone guidance during nervous system development in the insect embryo. A search of NBRF protein database revealed a significant homologous

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domain between TC1 and Fasciclin I from Grasshopper and Drosophila. One TC1 domain of 204 amino acids (amino acid residue 503-706) shared 30% identity with Grasshopper Fasciclin I, and shared 25% identity with Drosophila Fasciclin. Fig. 9 shows amino acid sequence homology between TC1 (SEQ ID NO:4) and Fasciclin I from Grasshopper (GrF) (SEQ ID NO:18) and Drosophila (DrF) (SEQ ID NO:19). Boxed amino acids are identical with at least one other amino acid at that same position.

It has been found that Fasciclin also contained four internal homologous domains, each consisting of approximately 150 amino acids. The domains of TC1 and Fasciclin I share some highly conserved amino acid stretches such as $\text{TXF} \frac{V}{A} \text{PTNXAF}$, and VXHVVDDXXLXP .

The most conserved sequence among TC1, Big-h3 and Fasciclin is $\text{TXF} \frac{A}{V} \text{PTNXA} \frac{F}{W}$. All four internal repeats in TC1 or Big-h3 or Fasciclin I also share the most conserved sequence $\text{TXF} \frac{A}{V} \text{P} \frac{T}{S} \text{NXA} \frac{F}{W}$. This sequence appears to be an important motif of this gene family.

Screening for antagonists to TC1 function.

The invention also includes methods of screening for agents which inhibit TC1 gene expression, whether such inhibition be at the transcriptional or translational level.

Screening methods, according to the invention, for agents which inhibit expression of the TC1 gene *in vitro* will include exposing a metastatic cell line in which TC1 mRNA is detectable in culture to an agent suspected of inhibiting production of the TC1 mRNA; and determining the level of TC1 mRNA in the exposed cell line, wherein a decrease in the level of TC1 mRNA after exposure of the cell line to the agent is indicative of inhibition of TC1 mRNA production.

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Alternatively, such screening methods may include *in vitro* screening of a metastatic cell line in which TC1 protein is detectable in culture to an agent suspected of inhibiting production of the TC1 protein; and determining the level of TC1 protein in the cell line, wherein a decrease in the level of TC1 protein after exposure of the cell line to the agent is indicative of inhibition of TC1 protein production.

The invention also encompasses *in vivo* methods of screening for agents which inhibit expression of the TC1 gene, comprising exposing a mammal having tumor cells in which TC1 mRNA or protein is detectable to an agent suspected of inhibiting production of TC1 mRNA or protein; and determining the level of TC1 mRNA or protein in tumor cells of the exposed mammal. A decrease in the level of TC1 mRNA or protein after exposure of the mammal to the agent is indicative of inhibition of TC1 gene expression.

According to the invention, agents can be screened *in vitro* or *in vivo* as follows. For *in vitro* screening, a metastatic cell line, e.g., JMN1B, may be cultured *in vitro* and exposed to an agent suspected of inhibiting TC1 expression in an amount and for a time sufficient to inhibit such expression. For *in vivo* screening, a mammal afflicted with a late stage cancer, particularly one of breast cancer, colon cancer, or cancer of the gastrointestinal tract, is exposed to the agent at a dosage and for a time sufficient to inhibit expression of TC1. A late stage cancer is defined by the Duke's stage of the cancer; i.e., late stage cancers correspond to Duke's stages 3-4. The amount or dosage of the agent which is effective to inhibit TC1 expression may be determined using serial dilutions of the agent. The level of TC1 mRNA or protein may be determined using an aliquot of cells from the cell culture or the *in vivo* tumor and performing Northern Blot analysis or Western Blot analysis, respectively. The agent will be considered inhibitory if the

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level of TC1 mRNA or protein decreases by more than 50%, and preferably more than 70-80%, relative to the same cell line which has not been exposed to the agent.

Examples of potential inhibitors of TC1 mRNA or protein production include but are not limited to antisense RNA, competitive inhibitors of the TC1 protein such as fragments of the TC1 protein itself, or antibodies to TC1 protein. Candidate TC1 inhibitory fragments include, but are not limited to, $T \frac{L}{Y} F \frac{A}{V} P \frac{T}{S} N \frac{E}{D} A \frac{F}{W}$ and $NG \frac{V}{A} \frac{I}{V} HX \frac{I}{V} \frac{D}{F}$.

Use of anatagonists to TC1 functions.

The invention also encompasses the treatment of late stage cancers by administration to a mammal afflicted with a late stage cancer one or more of the above-selected inhibitory agents. Late stage cancers, particularly those of the breast, colon, or gastrointestinal tract, are treated according to the invention by administering the inhibitory agent to a mammal afflicted with a late stage cancer in an amount and for a time sufficient to decrease the level of TC1 protein or mRNA.

The mode of administration may be intravenously, intraperitoneally, by intramuscular or intradermal injection, or orally. Administration may be by single dose, or may be continuous or intermittent. The dosage of inhibitory agent is that dosage which is effective to inhibit TC1 production, i.e., within the range of 10 μ g/kg body weight - 100 gm/kg body weight, preferably, within the range of 1 mg/kg body weight - 1 gm/kg body weight, most preferably 10-100 mg/kg body weight.

Production of monoclonal antibodies reactive with TC1.

An anti-TC1 antibody is produced according to Kohler and Milstein, Nature, 256:495-497 (1975), Eur. J. Immunol. 6:511-519 (1976), both of which are hereby incorporated by reference, using the TC1 protein or a fragment thereof as the

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immunizing antigen. Hybridomas produced by the above process are selected for anti-TC1 antibodies using the TC1 as an antigen in an ELISA assay. The single type of immunoglobulin produced by a such a hybridoma is specific for a single antigenic determinant, or epitope, on the TC1 antigen. Certain TC1-specific antibodies, for example, anti-TC1-1 produced by the hybridoma deposited with the American Type Culture Collection (ATCC) under the ATCC number HB 11481, are unique in that they recognize the TC1 protein, more specifically an epitope of the TC1 protein, in formaldehyde-fixed and paraffin-embedded tumor cells which bear TC1.

Deposits

The following samples were deposited on October 29, 1993, with the American Type Culture Collection (ATCC), 12301 Parklawn Drive, Rockville, MD 20852.

<u>Deposit</u>	<u>ATCC Accession No.</u>
TC1 gene in pBluescript plasmid DNA vector	75599
Hybridoma TC-1	HB 11481

Applicants' assignee, Dana-Farber Cancer Institute, Inc., represents that the ATCC is a depository affording permanence of the deposit and ready accessibility thereto by the public if a patent is granted. All restrictions on the availability to the public of the material so deposited will be irrevocably removed upon the granting of a patent. The material will be available during the pendency of the patent application to one determined by the Commissioner to be entitled thereto under 37 CFR 1.14 and 35 USC 122. The deposited material will be maintained with all the care necessary to keep it viable and uncontaminated for a period of at least five years after the most recent request for the furnishing of a sample of the deposited microorganism, and in any case, for a period of at least thirty (30) years after the date of deposit or for the enforceable life of the

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patent, whichever period is longer. Applicants' assignee acknowledges its duty to replace the deposit should the depository be unable to furnish a sample when requested due to the condition of the deposit.

5

OTHER EMBODIMENTS

10

The invention is not limited to those embodiments described herein, but may encompass modifications and variations which do not depart from the spirit of the invention. While the invention has been described in connection with specific embodiments thereof, it will be understood that further modifications are within the scope of the following claims.

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Chen, Lan Bo
 Bao, Shideng
 Liu, Yuan

(ii) TITLE OF INVENTION: A NOVEL TUMOR MARKER AND NOVEL METHOD OF
 ISOLATING SAME

(iii) NUMBER OF SEQUENCES: 19

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
(B) STREET: Ten Post Office Square
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(D) STATE: Massachusetts
(E) COUNTRY: USA
(F) ZIP: 02109

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/146,488
(B) FILING DATE: 29-OCT-1993
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Heine, Holliday C.
(B) REGISTRATION NUMBER: 34,346
(C) REFERENCE/DOCKET NUMBER: DFCI-333XX

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 636 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..636

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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	1 5 10 15	
5	GAC CGT GTG CTT ACA CAA ATT GGT ACC TCA ATT CAA GAC TTC ATT GAA	96
	Asp Arg Val Leu Thr Gln Ile Gly Thr Ser Ile Gln Asp Phe Ile Glu	
	20 25 30	
	GCA GAA GAT GAC CTT TCA TCT TTT AGA GCA GCT GCC ATC ACA TCG GAC	144
	Ala Glu Asp Asp Leu Ser Ser Phe Arg Ala Ala Ala Ile Thr Ser Asp	
10	35 40 45	
	ATA TTG GAG GCC CTT GGA AGA GAC GGT CAC TTC ACA CTC TTT GCT CCC	192
	Ile Leu Glu Ala Leu Gly Arg Asp Gly His Phe Thr Leu Phe Ala Pro	
	50 55 60	
	ACC AAT GAG GCT TTT GAG AAA CTT CCA CGA GGT GTC CTA GAA AGG ATC	240
15	Thr Asn Glu Ala Phe Glu Lys Leu Pro Arg Gly Val Leu Glu Arg Ile	
	65 70 75 80	
	ATG GGA GAC AAA GTG GCT TCC GAA GCT CTT ATG AAG TAC CAC ATC TTA	288
	Met Gly Asp Lys Val Ala Ser Glu Ala Leu Met Lys Tyr His Ile Leu	
	85 90 95	
20	AAT ACT CTC CAG TGT TCT GAG TCT ATT ATG GGA GGA GCA GTC TTT GAG	336
	Asn Thr Leu Gln Cys Ser Glu Ser Ile Met Gly Gly Ala Val Phe Glu	
	100 105 110	
	ACG CTG GAA GGA AAT ACA ATT GAG ATA GGA TGT GAC GGT GAC AGT ATA	384
	Thr Leu Glu Gly Asn Thr Ile Glu Ile Gly Cys Asp Gly Asp Ser Ile	
25	115 120 125	
	ACA GTA AAT GGA ATC AAA ATG GTG AAC AAA AAG GAT ATT GTG ACA AAT	432
	Thr Val Asn Gly Ile Lys Met Val Asn Lys Lys Asp Ile Val Thr Asn	
	130 135 140	
	AAT GGT GTG ATC CAT TTG ATT GAT CAG GTC CTA ATT CCT GAT TCT GCC	480
30	Asn Gly Val Ile His Leu Ile Asp Gln Val Leu Ile Pro Asp Ser Ala	
	145 150 155 160	
	AAA CAA GTT ATT GAG CTG GCT GGA AAA CAG CAA ACC ACC TTC ACG GAT	528
	Lys Gln Val Ile Glu Leu Ala Gly Lys Gln Gln Thr Thr Phe Thr Asp	
	165 170 175	
35	CTT GTG GCC CAA TTA GGC TTG GCA TCT GCT CTG AGG CCA GAT GGA GAA	576
	Leu Val Ala Gln Leu Gly Leu Ala Ser Ala Leu Arg Pro Asp Gly Glu	
	180 185 190	
	TAC ACT TTG CTG GCA CCT GTG AAT AAT GCA TTT TCT GAT GAT ACT CTC	624
	Tyr Thr Leu Leu Ala Pro Val Asn Asn Ala Phe Ser Asp Asp Thr Leu	
40	195 200 205	
	AGC ATG GAT CAG	636
	Ser Met Asp Gln	
	210	

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 212 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Leu Ile His Gly Asn Gln Ile Ala Thr Asn Gly Val Val His Val Ile
 1 5 10 15
 Asp Arg Val Leu Thr Gln Ile Gly Thr Ser Ile Gln Asp Phe Ile Glu
 20 25 30
 Ala Glu Asp Asp Leu Ser Ser Phe Arg Ala Ala Ala Ile Thr Ser Asp
 35 40 45
 Ile Leu Glu Ala Leu Gly Arg Asp Gly His Phe Thr Leu Phe Ala Pro
 50 55 60
 Thr Asn Glu Ala Phe Glu Lys Leu Pro Arg Gly Val Leu Glu Arg Ile
 65 70 75 80
 Met Gly Asp Lys Val Ala Ser Glu Ala Leu Met Lys Tyr His Ile Leu
 85 90 95
 Asn Thr Leu Gln Cys Ser Glu Ser Ile Met Gly Gly Ala Val Phe Glu
 100 105 110
 Thr Leu Glu Gly Asn Thr Ile Glu Ile Gly Cys Asp Gly Asp Ser Ile
 115 120 125
 Thr Val Asn Gly Ile Lys Met Val Asn Lys Lys Asp Ile Val Thr Asn
 130 135 140
 Asn Gly Val Ile His Leu Ile Asp Gln Val Leu Ile Pro Asp Ser Ala
 145 150 155 160
 Lys Gln Val Ile Glu Leu Ala Gly Lys Gln Gln Thr Thr Phe Thr Asp
 165 170 175
 Leu Val Ala Gln Leu Gly Leu Ala Ser Ala Leu Arg Pro Asp Gly Glu
 180 185 190
 Tyr Thr Leu Ala Pro Val Asn Asn Ala Phe Ser Asp Asp Thr Leu
 195 200 205
 Ser Met Asp Gln
 210

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3126 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

- 34 -

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 43..2376

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

5	GCCACCATGT AGCCCGCGTC ACCGTTCTGC GCATTCCGCA GC ATG GCT CTG CCT	54
	Met Ala Leu Pro	
	1	
10	GCC CGA ATC CTC GCT CTG GCC CTC GCA CTG GCG CTC GGA CCC GCC GTG	102
	Ala Arg Ile Leu Ala Leu Ala Leu Ala Leu Ala Leu Gly Pro Ala Val	
	5 10 15 20	
	ACA CTG GCC AAC CCG GCG AGA ACG CCG TAC GAG CTG GTA CTC CAG AAG	150
	Thr Leu Ala Asn Pro Ala Arg Thr Pro Tyr Glu Leu Val Leu Gln Lys	
	25 30 35	
15	AGC TCG GCA CGA GGG GGT CCG GAC CAA GGC CCA AAT GTC TGT GCC CTT	198
	Ser Ser Ala Arg Gly Gly Arg Asp Gln Gly Pro Asn Val Cys Ala Leu	
	40 45 50	
	CAA CAG ATT TTG GGC ACC AAA AAG AAA TAC TTC AGC ACT TGT AAG AAC	246
	Gln Gln Ile Leu Gly Thr Lys Lys Lys Tyr Phe Ser Thr Cys Lys Asn	
20	55 60 65	
	TGG TAT AAA AAG TCC ATC TGT GGA CAG AAA ACG ACT GTG TTA TAT GAA	294
	Trp Tyr Lys Lys Ser Ile Cys Gly Gln Lys Thr Thr Val Leu Tyr Glu	
	70 75 80	
25	TGT TGC CCT GGT TAT ATG AGA ATG GAA GGA ATG AAA GGC TGC CCA GCA	342
	Cys Cys Pro Gly Tyr Met Arg Met Glu Gly Met Lys Gly Cys Pro Ala	
	85 90 95 100	
	GTT TTG CCC ATT GAC CAT GTT TAT GGC ACT CTG GGC ATC GTG GGA GCC	390
	Val Leu Pro Ile Asp His Val Tyr Gly Thr Leu Gly Ile Val Gly Ala	
	105 110 115	
30	ACC ACA ACG CAG CGC TAT TCT GAC GCC TCA AAA CTG AGG GAG GAG ATC	438
	Thr Thr Thr Gln Arg Tyr Ser Asp Ala Ser Lys Leu Arg Glu Glu Ile	
	120 125 130	
	GAG GGA AAG GGA TCC TTC ACT TAC TTT GCA CCG AGT AAT GAG GCT TGG	486
	Glu Gly Lys Gly Ser Phe Thr Tyr Phe Ala Pro Ser Asn Glu Ala Trp	
35	135 140 145	
	GAC AAC TTG GAT TCT GAT ATC CGT AGA GGT TTG GAG AGC AAC GTG AAT	534
	Asp Asn Leu Asp Ser Asp Ile Arg Arg Gly Leu Glu Ser Asn Val Asn	
	150 155 160	
40	GTT GAA TTA CTG AAT GCT TTA CAT AGT CAC ATG ATT AAT AAG AGA ATG	582
	Val Glu Leu Leu Asn Ala Leu His Ser His Met Ile Asn Lys Arg Met	
	165 170 175 180	
	TTG ACC AAG GAC TTA AAA AAT GGC ATG ATT ATT CCT TCA ATG TAT AAC	630
	Leu Thr Lys Asp Leu Lys Asn Gly Met Ile Ile Pro Ser Met Tyr Asn	
	185 190 195	

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	AAT TTG GGG CTT TTC ATT AAC CAT TAT CCT AAT GGG GTT GTC ACT GTT	678
	Asn Leu Gly Leu Phe Ile Asn His Tyr Pro Asn Gly Val Val Thr Val	
	200 205 210	
5	AAT TGT GCT CGA ATC ATC CAT GGG AAC CAG ATT GCA ACA AAT GGT GTT	726
	Asn Cys Ala Arg Ile Ile His Gly Asn Gln Ile Ala Thr Asn Gly Val	
	215 220 225	
	GTC CAT GTC ATT GAC CGT GTG CTT ACA CAA ATT GGT ACC TCA ATT CAA	774
	Val His Val Ile Asp Arg Val Leu Thr Gln Ile Gly Thr Ser Ile Gln	
	230 235 240	
10	GAC TTC ATT GAA GCA GAA GAT GAC CTT TCA TCT TTT AGA GCA GCT GCC	822
	Asp Phe Ile Glu Ala Glu Asp Asp Leu Ser Ser Phe Arg Ala Ala Ala	
	245 250 255 260	
	ATC ACA TCG GAC ATA TTG GAG GCC CTT GGA AGA GAC GGT CAC TTC ACA	870
	Ile Thr Ser Asp Ile Leu Glu Ala Leu Gly Arg Asp Gly His Phe Thr	
15	265 270 275	
	CTC TTT GCT CCC ACC AAT GAG GCT TTT GAG AAA CTT CCA CGA GGT GTC	918
	Leu Phe Ala Pro Thr Asn Glu Ala Phe Glu Lys Leu Pro Arg Gly Val	
	280 285 290	
20	CTA GAA AGG ATC ATG GGA GAC AAA GTG GCT TCC GAA GCT CTT ATG AAG	966
	Leu Glu Arg Ile Met Gly Asp Lys Val Ala Ser Glu Ala Leu Met Lys	
	295 300 305	
	TAC CAC ATC TTA AAT ACT CTC CAG TGT TCT GAG TCT ATT ATG GGA GGA	1014
	Tyr His Ile Leu Asn Thr Leu Gln Cys Ser Glu Ser Ile Met Gly Gly	
	310 315 320	
25	GCA GTC TTT GAG ACG CTG GAA GGA AAT ACA ATT GAG ATA GGA TGT GAC	1062
	Ala Val Phe Glu Thr Leu Glu Gly Asn Thr Ile Glu Ile Gly Cys Asp	
	325 330 335 340	
	GGT GAC AGT ATA ACA GTA AAT GGA ATC AAA ATG GTG AAC AAA AAG GAT	1110
	Gly Asp Ser Ile Thr Val Asn Gly Ile Lys Met Val Asn Lys Lys Asp	
30	345 350 355	
	ATT GTG ACA AAT AAT GGT GTG ATC CAT TTG ATT GAT CAG GTC CTA ATT	1158
	Ile Val Thr Asn Asn Gly Val Ile His Leu Ile Asp Gln Val Leu Ile	
	360 365 370	
35	CCT GAT TCT GCC AAA CAA GTT ATT GAG CTG GCT GGA AAA CAG CAA ACC	1206
	Pro Asp Ser Ala Lys Gln Val Ile Glu Leu Ala Gly Lys Gln Gln Thr	
	375 380 385	
	ACC TTC ACG GAT CTT GTG GCC CAA TTA GGC TTG GCA TCT GCT CTG AGG	1254
	Thr Phe Thr Asp Leu Val Ala Gln Leu Gly Leu Ala Ser Ala Leu Arg	
	390 395 400	
40	CCA GAT GGA GAA TAC ACT TTG CTG GCA CCT GTG AAT AAT GCA TTT TCT	1302
	Pro Asp Gly Glu Tyr Thr Leu Leu Ala Pro Val Asn Asn Ala Phe Ser	
	405 410 415 420	

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	GAT GAT ACT CTC AGC ATG GAT CAG CGC CTC CTT AAA TTA ATT CTG CAG	1350
	Asp Asp Thr Leu Ser Met Asp Gln Arg Leu Leu Lys Leu Ile Leu Gln	
	425 430 435	
5	AAT CAC ATA TTG AAA GTA AAA GTT GGC CTT AAT GAG CTT TAC AAC GGG	1398
	Asn His Ile Leu Lys Val Lys Val Gly Leu Asn Glu Leu Tyr Asn Gly	
	440 445 450	
	CAA ATA CTG GAA ACC ATC GGA GGC AAA CAG CTC AGA GTC TTC GTA TAT	1446
	Gln Ile Leu Glu Thr Ile Gly Gly Lys Gln Leu Arg Val Phe Val Tyr	
	455 460 465	
10	CGT ACA GCT GTC TGC ATT GAA AAT TCA TGC ATG GAG AAA GGG AGT AAG	1494
	Arg Thr Ala Val Cys Ile Glu Asn Ser Cys Met Glu Lys Gly Ser Lys	
	470 475 480	
	CAA GGG AGA AAC GGT GCG ATT CAC ATA TTC CGC GAG ATC ATC AAG CCA	1542
	Gln Gly Arg Asn Gly Ala Ile His Ile Phe Arg Glu Ile Ile Lys Pro	
15	485 490 495 500	
	GCA GAG AAA TCC CTC CAT GAA AAG TTA AAA CAA GAT AAG CGC TTT ACG	1590
	Ala Glu Lys Ser Leu His Glu Lys Leu Lys Gln Asp Lys Arg Phe Thr	
	505 510 515	
20	ACC TTC CTC AGC CTA CTT GAA GCT GCA GAC TTG AAA GAG CTC CTG ACA	1638
	Thr Phe Leu Ser Leu Leu Glu Ala Ala Asp Leu Lys Glu Leu Leu Thr	
	520 525 530	
	CAA CCT GGA GAC TGG ACA TTA TTT GTG CCA ACC AAT GAT GCT TTT AAG	1686
	Gln Pro Gly Asp Trp Thr Leu Phe Val Pro Thr Asn Asp Ala Phe Lys	
	535 540 545	
25	GGA ATG ACT AGT GAA GAA AAA GAA ATT CTG ATA CGG GAC AAA AAT GCT	1734
	Gly Met Thr Ser Glu Glu Lys Glu Ile Leu Ile Arg Asp Lys Asn Ala	
	550 555 560	
	CTT CAA AAC ATC ATT CTT TAT CAC CTG ACA CCA GGA GTT TTC ATT GGA	1782
	Leu Gln Asn Ile Ile Leu Tyr His Leu Thr Pro Gly Val Phe Ile Gly	
30	565 570 575 580	
	AAA GGA TTT GAA CCT GGT GTT ACT AAC ATT TTA AAG ACC ACA CAA GGA	1830
	Lys Gly Phe Glu Pro Gly Val Thr Asn Ile Leu Lys Thr Thr Gln Gly	
	585 590 595	
35	AGC AAA ATC TTT CTG AAA GAA GTA AAT GAT ACA CTT CTG GTG AAT GAA	1878
	Ser Lys Ile Phe Leu Lys Glu Val Asn Asp Thr Leu Leu Val Asn Glu	
	600 605 610	
	TTG AAA TCA AAA GAA TCT GAC ATC ATG ACA ACA AAT GGT GTA ATT CAT	1926
	Leu Lys Ser Lys Glu Ser Asp Ile Met Thr Thr Asn Gly Val Ile His	
	615 620 625	
40	GTT GTA GAT AAA CTC CTC TAT CCA GCA GAC ACA CCT GTT GGA AAT GAT	1974
	Val Val Asp Lys Leu Leu Tyr Pro Ala Asp Thr Pro Val Gly Asn Asp	
	630 635 640	

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	CAA CTG CTG GAA ATA CTT AAT AAA TTA ATC AAA TAC ATC CAA ATT AAG	2022
	Gln Leu Leu Glu Ile Leu Asn Lys Leu Ile Lys Tyr Ile Gln Ile Lys	
	645 650 655 660	
5	TTT GTT CGT GGT AGC ACC TTC AAA GAA ATC CCC GTG ACT GTC TAT AGA	2070
	Phe Val Arg Gly Ser Thr Phe Lys Glu Ile Pro Val Thr Val Tyr Arg	
	665 670 675	
	CCC ACA CTA ACA AAA GTC AAA ATT GAA GGT GAA CCT GAA TTC AGA CTG	2118
	Pro Thr Leu Thr Lys Val Lys Ile Glu Gly Glu Pro Glu Phe Arg Leu	
	680 685 690	
10	ATT AAA GAA GGT GAA ACA ATA ACT GAA GTG ATC CAT GGA GAG CCA ATT	2166
	Ile Lys Glu Gly Glu Thr Ile Thr Glu Val Ile His Gly Glu Pro Ile	
	695 700 705	
	ATT AAA AAA TAC ACC AAA ATC ATT GAT GGA GTG CCT GTG GAA ATA ACT	2214
	Ile Lys Lys Tyr Thr Lys Ile Ile Asp Gly Val Pro Val Glu Ile Thr	
15	710 715 720	
	GAA AAA GAG ACA CGA GAA GAA CGA ATC ATT ACA GGT CCT GAA ATA AAA	2262
	Glu Lys Glu Thr Arg Glu Glu Arg Ile Ile Thr Gly Pro Glu Ile Lys	
	725 730 735 740	
20	TAC ACT AGG ATT TCT ACT GGA GGT GGA GAA ACA GAA GAA ACT CTG AAG	2310
	Tyr Thr Arg Ile Ser Thr Gly Gly Gly Glu Thr Glu Glu Thr Leu Lys	
	745 750 755	
	AAA TTG TTA CAA GAA GAC ACA CCC GTG AGG AAG TTG CAA GCC AAC AAA	2358
	Lys Leu Leu Gln Glu Asp Thr Pro Val Arg Lys Leu Gln Ala Asn Lys	
	760 765 770	
25	AAA AGT TCA AGG ATC TAGAAGACGA TTAAGGGAAG GTCGTTCTCA GTGAAAATCC	2413
	Lys Ser Ser Arg Ile	
	775	
	AAAAACCAGA AAAAAATGTT TATACAACCC TAAGTCAATA ACCTGACCTT AGAAAATTGT	2473
30	GAGAGCCAAG TTGACTTCAG GAACTGAAAC ATCAGCACAA AGAAGCAATC ATCAAATAAT	2533
	TCTGAACACA AATTTAATAT TTTTTTTTCT GAATGAGAAA CATGAGGGAA ATTGTGGAGT	2593
	TAGCCTCCTG TGGTAAAGGA ATTGAAGAAA ATATAACACC TTACACCCTT TTTCATCTTG	2653
	ACATTAAAAG TTCTGGCTAA CTTTGGAATC CATTAGAGAA AAATCCTTGT CACCAGATTC	2713
	ATTACAATTC AAATCGAAGA GTTGTGAACT GTTATCCCAT TGAAAAGACC GAGCCTTGTA	2773
	TGTATGTTAT GGATACATAA AATGCACGCA AGCCATTATC TCTCCATGGG AAGCTAAGTT	2833
35	ATAAAAATAG GTGCTTGGTG TACAAAACCTT TTTATGATCA AAAGGCTTTG CACATTTCTA	2893
	TATGAGTGGG TTTACTGGTA AATTATGTTA TTTTTTACAA CTAATTTTGT ACTCTCAGAA	2953
	TGTTTGTTCAT ATGCTTCTTG CAATGCATAT TTTTAAATCT CAAACGTTTC AATAAAACCA	3013
	TTTTTCAGAT ATAAAGAGAA TTAATTCAAA TTGAGTAATT CAGAAAAACT CAAGATTTAA	3073
	GTAAAAAGT GGTGTTGGACT TGGAATAGG ACTTTATAACC TCTTTCTCGT GCC	3126

40

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 777 amino acids

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(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

5	Met	Ala	Leu	Pro	Ala	Arg	Ile	Leu	Ala	Leu	Ala	Leu	Ala	Leu	Ala	Leu	
	1				5					10					15		
	Gly	Pro	Ala	Val	Thr	Leu	Ala	Asn	Pro	Ala	Arg	Thr	Pro	Tyr	Glu	Leu	
				20					25					30			
	Val	Leu	Gln	Lys	Ser	Ser	Ala	Arg	Gly	Gly	Arg	Asp	Gln	Gly	Pro	Asn	
10			35					40					45				
	Val	Cys	Ala	Leu	Gln	Gln	Ile	Leu	Gly	Thr	Lys	Lys	Lys	Tyr	Phe	Ser	
		50					55					60					
	Thr	Cys	Lys	Asn	Trp	Tyr	Lys	Lys	Ser	Ile	Cys	Gly	Gln	Lys	Thr	Thr	
	65				70					75					80		
15	Val	Leu	Tyr	Glu	Cys	Cys	Pro	Gly	Tyr	Met	Arg	Met	Glu	Gly	Met	Lys	
				85				90					95				
	Gly	Cys	Pro	Ala	Val	Leu	Pro	Ile	Asp	His	Val	Tyr	Gly	Thr	Leu	Gly	
			100					105					110				
20	Ile	Val	Gly	Ala	Thr	Thr	Thr	Gln	Arg	Tyr	Ser	Asp	Ala	Ser	Lys	Leu	
		115					120					125					
	Arg	Glu	Glu	Ile	Glu	Gly	Lys	Gly	Ser	Phe	Thr	Tyr	Phe	Ala	Pro	Ser	
	130					135					140						
	Asn	Glu	Ala	Trp	Asp	Asn	Leu	Asp	Ser	Asp	Ile	Arg	Arg	Gly	Leu	Glu	
	145				150				155					160			
25	Ser	Asn	Val	Asn	Val	Glu	Leu	Leu	Asn	Ala	Leu	His	Ser	His	Met	Ile	
				165					170					175			
	Asn	Lys	Arg	Met	Leu	Thr	Lys	Asp	Leu	Lys	Asn	Gly	Met	Ile	Ile	Pro	
			180					185				190					
	Ser	Met	Tyr	Asn	Asn	Leu	Gly	Leu	Phe	Ile	Asn	His	Tyr	Pro	Asn	Gly	
30		195				200					205						
	Val	Val	Thr	Val	Asn	Cys	Ala	Arg	Ile	Ile	His	Gly	Asn	Gln	Ile	Ala	
		210				215					220						
	Thr	Asn	Gly	Val	Val	His	Val	Ile	Asp	Arg	Val	Leu	Thr	Gln	Ile	Gly	
	225				230				235					240			
35	Thr	Ser	Ile	Gln	Asp	Phe	Ile	Glu	Ala	Glu	Asp	Asp	Leu	Ser	Ser	Phe	
				245				250					255				
	Arg	Ala	Ala	Ala	Ile	Thr	Ser	Asp	Ile	Leu	Glu	Ala	Leu	Gly	Arg	Asp	
			260					265					270				
	Gly	His	Phe	Thr	Leu	Phe	Ala	Pro	Thr	Asn	Glu	Ala	Phe	Glu	Lys	Leu	
40			275					280				285					
	Pro	Arg	Gly	Val	Leu	Glu	Arg	Ile	Met	Gly	Asp	Lys	Val	Ala	Ser	Glu	
		290				295					300						
	Ala	Leu	Met	Lys	Tyr	His	Ile	Leu	Asn	Thr	Leu	Gln	Cys	Ser	Glu	Ser	
	305				310						315				320		

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	Ile Met Gly Gly Ala Val Phe Glu Thr Leu Glu Gly Asn Thr Ile Glu	
	325	330 335
	Ile Gly Cys Asp Gly Asp Ser Ile Thr Val Asn Gly Ile Lys Met Val	
	340	345 350
5	Asn Lys Lys Asp Ile Val Thr Asn Asn Gly Val Ile His Leu Ile Asp	
	355	360 365
	Gln Val Leu Ile Pro Asp Ser Ala Lys Gln Val Ile Glu Leu Ala Gly	
	370	375 380
10	Lys Gln Gln Thr Thr Phe Thr Asp Leu Val Ala Gln Leu Gly Leu Ala	
	385	390 395 400
	Ser Ala Leu Arg Pro Asp Gly Glu Tyr Thr Leu Leu Ala Pro Val Asn	
	405	410 415
	Asn Ala Phe Ser Asp Asp Thr Leu Ser Met Asp Gln Arg Leu Leu Lys	
	420	425 430
15	Leu Ile Leu Gln Asn His Ile Leu Lys Val Lys Val Gly Leu Asn Glu	
	435	440 445
	Leu Tyr Asn Gly Gln Ile Leu Glu Thr Ile Gly Gly Lys Gln Leu Arg	
	450	455 460
20	Val Phe Val Tyr Arg Thr Ala Val Cys Ile Glu Asn Ser Cys Met Glu	
	465	470 475 480
	Lys Gly Ser Lys Gln Gly Arg Asn Gly Ala Ile His Ile Phe Arg Glu	
	485	490 495
	Ile Ile Lys Pro Ala Glu Lys Ser Leu His Glu Lys Leu Lys Gln Asp	
	500	505 510
25	Lys Arg Phe Thr Thr Phe Leu Ser Leu Leu Glu Ala Ala Asp Leu Lys	
	515	520 525
	Glu Leu Leu Thr Gln Pro Gly Asp Trp Thr Leu Phe Val Pro Thr Asn	
	530	535 540
30	Asp Ala Phe Lys Gly Met Thr Ser Glu Glu Lys Glu Ile Leu Ile Arg	
	545	550 555 560
	Asp Lys Asn Ala Leu Gln Asn Ile Ile Leu Tyr His Leu Thr Pro Gly	
	565	570 575
	Val Phe Ile Gly Lys Gly Phe Glu Pro Gly Val Thr Asn Ile Leu Lys	
	580	585 590
35	Thr Thr Gln Gly Ser Lys Ile Phe Leu Lys Glu Val Asn Asp Thr Leu	
	595	600 605
	Leu Val Asn Glu Leu Lys Ser Lys Glu Ser Asp Ile Met Thr Thr Asn	
	610	615 620
40	Gly Val Ile His Val Val Asp Lys Leu Leu Tyr Pro Ala Asp Thr Pro	
	625	630 635 640
	Val Gly Asn Asp Gln Leu Leu Glu Ile Leu Asn Lys Leu Ile Lys Tyr	
	645	650 655
	Ile Gln Ile Lys Phe Val Arg Gly Ser Thr Phe Lys Glu Ile Pro Val	
	660	665 670

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Thr Val Tyr Arg Pro Thr Leu Thr Lys Val Lys Ile Glu Gly Glu Pro
 675 680 685
 Glu Phe Arg Leu Ile Lys Glu Gly Glu Thr Ile Thr Glu Val Ile His
 690 695 700
 5 Gly Glu Pro Ile Ile Lys Lys Tyr Thr Lys Ile Ile Asp Gly Val Pro
 705 710 715 720
 Val Glu Ile Thr Glu Lys Glu Thr Arg Glu Glu Arg Ile Ile Thr Gly
 725 730 735
 Pro Glu Ile Lys Tyr Thr Arg Ile Ser Thr Gly Gly Gly Glu Thr Glu
 10 740 745 750
 Glu Thr Leu Lys Lys Leu Leu Gln Glu Asp Thr Pro Val Arg Lys Leu
 755 760 765
 Gln Ala Asn Lys Lys Ser Ser Arg Ile
 770 775

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TGTCCAGATG

10

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TGTCCAGATG C

11

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 base pairs

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- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: cDNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
TGTC CAGATG AC
12

10 (2) INFORMATION FOR SEQ ID NO:8:

 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: cDNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
20 TGTC CAGATA
10

 (2) INFORMATION FOR SEQ ID NO:9:

 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: cDNA
 (iii) HYPOTHETICAL: NO
30 (iv) ANTI-SENSE: NO
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
TGTC CAGACG
10

 (2) INFORMATION FOR SEQ ID NO:10:

 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: cDNA
 (iii) HYPOTHETICAL: NO

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(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TGTCCAGCCG

10

5

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

10

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

15

TGTCCCGCCG

10

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 base pairs

20

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

25

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TGCCCGGCCG

10

(2) INFORMATION FOR SEQ ID NO:13:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TGATGCACTC

40

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(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TGAGCTACTC

10

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TGACTGACTC

10

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CTGATCCATG

10

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 683 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

5 (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

	Met	Ala	Leu	Phe	Val	Arg	Leu	Leu	Ala	Leu	Ala	Leu	Ala	Leu	Ala	Leu	
	1				5					10					15		
	Gly	Pro	Ala	Ala	Thr	Leu	Ala	Gly	Pro	Ala	Lys	Ser	Pro	Tyr	Gln	Leu	
10					20				25					30			
	Pro	Leu	Gln	His	Ser	Arg	Leu	Arg	Gly	Arg	Gln	His	Gly	Pro	Asn	Val	
					35				40					45			
	Cys	Ala	Val	Thr	Lys	Val	Ile	Gly	Thr	Asn	Arg	Lys	Tyr	Phe	Thr	Asn	
					50				55					60			
15	Cys	Lys	Gln	Trp	Tyr	Gln	Arg	Lys	Ile	Cys	Gly	Lys	Ser	Thr	Val	Ile	
					65				70					75		80	
	Ser	Tyr	Glu	Cys	Cys	Pro	Gly	Tyr	Glu	Lys	Val	Pro	Gly	Glu	Lys	Gly	
					85				90					95			
	Cys	Pro	Ala	Ala	Leu	Pro	Leu	Ser	Asn	Leu	Tyr	Glu	Thr	Leu	Gly	Val	
20					100				105					110			
	Val	Gly	Ser	Thr	Thr	Thr	Gln	Leu	Tyr	Thr	Asp	Arg	Thr	Glu	Lys	Leu	
					115				120					125			
	Arg	Pro	Glu	Met	Glu	Gly	Pro	Gly	Ser	Phe	Thr	Ile	Phe	Ala	Pro	Ser	
					130				135					140			
25	Asn	Glu	Ala	Trp	Ala	Ser	Leu	Pro	Ala	Glu	Val	Leu	Val	Ser	Leu	Val	
					145				150					155		160	
	Ser	Asn	Val	Asn	Ile	Glu	Leu	Leu	Asn	Ala	Leu	Arg	Tyr	His	Met	Val	
					165				170					175			
	Gly	Arg	Arg	Val	Leu	Thr	Asp	Glu	Leu	Lys	His	Gly	Met	Thr	Leu	Thr	
30					180				185					190			
	Ser	Met	Tyr	Gln	Asn	Ser	Asn	Ile	Gln	Ile	His	His	Tyr	Pro	Asn	Gly	
					195				200					205			
	Ile	Val	Thr	Val	Asn	Cys	Ala	Arg	Leu	Leu	Lys	Ala	Asp	His	His	Ala	
					210				215					220			
35	Thr	Asn	Gly	Val	Val	His	Leu	Ile	Asp	Lys	Val	Ile	Ser	Thr	Ile	Thr	
					225				230					235		240	
	Asn	Asn	Ile	Gln	Gln	Ile	Ile	Glu	Ile	Glu	Asp	Thr	Phe	Glu	Thr	Leu	
					245				250					255			
	Arg	Ala	Ala	Val	Ala	Ala	Ser	Gly	Leu	Asn	Thr	Met	Leu	Glu	Gly	Asn	
40					260				265					270			
	Gly	Gln	Tyr	Thr	Leu	Leu	Ala	Pro	Thr	Asn	Glu	Ala	Phe	Glu	Lys	Ile	
					275				280					285			
	Pro	Ser	Glu	Thr	Leu	Asn	Arg	Ile	Leu	Gly	Asp	Pro	Glu	Ala	Leu	Arg	
					290				295					300			

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	Asp	Leu	Leu	Asn	Asn	His	Ile	Leu	Lys	Ser	Ala	Met	Cys	Ala	Glu	Ala	
	305					310					315					320	
	Ile	Val	Ala	Gly	Leu	Ser	Val	Glu	Thr	Leu	Glu	Gly	Thr	Thr	Leu	Glu	
				325						330					335		
5	Val	Gly	Cys	Ser	Gly	Asp	Met	Leu	Thr	Ile	Asn	Gly	Lys	Ala	Ile	Ile	
				340					345					350			
	Ser	Asn	Lys	Asp	Ile	Leu	Ala	Thr	Asn	Gly	Val	Ile	His	Tyr	Ile	Asp	
			355					360					365				
10	Glu	Leu	Leu	Ile	Pro	Asp	Ser	Ala	Lys	Thr	Leu	Phe	Glu	Leu	Ala	Ala	
	370					375					380						
	Glu	Ser	Asp	Val	Ser	Thr	Ala	Ile	Asp	Leu	Phe	Arg	Gln	Ala	Gly	Leu	
	385					390				395					400		
	Gly	Asn	His	Leu	Ser	Gly	Ser	Glu	Arg	Leu	Thr	Leu	Leu	Ala	Pro	Leu	
				405				410					415				
15	Asn	Ser	Val	Phe	Lys	Asp	Gly	Thr	Pro	Pro	Ile	Asp	Ala	His	Thr	Arg	
			420					425					430				
	Asn	Leu	Leu	Arg	Asn	His	Ile	Ile	Lys	Asp	Gln	Leu	Ala	Ser	Lys	Tyr	
			435					440					445				
20	Leu	Tyr	His	Gly	Gln	Thr	Leu	Glu	Thr	Leu	Gly	Gly	Lys	Lys	Leu	Arg	
	450					455				460							
	Val	Phe	Val	Tyr	Arg	Asn	Ser	Leu	Cys	Ile	Glu	Asn	Ser	Cys	Ile	Ala	
	465				470				475					480			
	Ala	His	Asp	Lys	Arg	Gly	Arg	Tyr	Gly	Thr	Leu	Phe	Thr	Met	Asp	Arg	
				485				490					495				
25	Val	Leu	Thr	Pro	Pro	Met	Gly	Thr	Val	Met	Asp	Val	Leu	Lys	Gly	Asp	
			500					505				510					
	Asn	Arg	Phe	Ser	Met	Leu	Val	Ala	Ala	Ile	Gln	Ser	Ala	Gly	Leu	Thr	
			515					520				525					
30	Glu	Thr	Leu	Asn	Arg	Glu	Gly	Val	Tyr	Thr	Val	Phe	Ala	Pro	Thr	Asn	
	530					535				540							
	Glu	Ala	Phe	Arg	Ala	Leu	Pro	Pro	Arg	Glu	Ser	Arg	Arg	Leu	Leu	Gly	
	545				550				555					560			
	Asp	Ala	Lys	Glu	Leu	Ala	Asn	Ile	Leu	Lys	Tyr	His	Ile	Gly	Asp	Glu	
				565				570					575				
35	Ile	Leu	Val	Ser	Gly	Gly	Ile	Gly	Ala	Leu	Val	Arg	Leu	Lys	Ser	Leu	
			580					585				590					
	Gln	Gly	Asp	Lys	Leu	Glu	Val	Ser	Leu	Lys	Asn	Asn	Val	Val	Ser	Val	
			595					600				605					
40	Asn	Lys	Glu	Pro	Val	Ala	Glu	Pro	Asp	Ile	Met	Ala	Thr	Asn	Gly	Val	
	610					615				620							
	Val	His	Val	Ile	Thr	Asn	Val	Leu	Gln	Pro	Pro	Ala	Asn	Arg	Pro	Gln	
	625				630				635				640				
	Glu	Arg	Gly	Asp	Glu	Leu	Ala	Asp	Ser	Ala	Leu	Glu	Ile	Phe	Lys	Gln	
				645				650					655				

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Ala Ser Ala Phe Ser Arg Ala Ser Gln Arg Ser Val Arg Leu Ala Val
 660 665 670
 Pro Tyr Gln Lys Leu Leu Glu Arg Met Lys His
 675 680

5 (2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 206 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

10 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Gly Glu Lys Ser Leu Glu Tyr Lys Ile Arg Asp Asp Pro Asp Leu Ser
 1 5 10 15
 Gln Phe Tyr Ser Trp Leu Glu His Asn Glu Val Ala Asn Ser Thr Leu
 20 25 30
 Gln Leu Arg Gln Val Thr Val Phe Ala Pro Thr Asn Leu Ala Gln Phe
 35 40 45
 Asn Tyr Lys Ala Arg Asp Gly Asp Glu Asn Ile Ile Leu Tyr His Met
 50 55 60
 Thr Asn Leu Ala His Ser Leu Asp Gln Leu Gly His Lys Val Asn Ser
 25 65 70 75 80
 Glu Leu Asp Gly Asn Pro Pro Leu Trp Ile Thr Arg Arg Arg Asp Thr
 85 90 95
 Ile Phe Val Asn Asn Ala Arg Val Leu Thr Glu Arg Ser Asn Tyr Glu
 100 105 110
 Ala Val Asn Arg His Gly Lys Lys Gln Val Leu His Val Val Asp Ser
 30 115 120 125
 Val Leu Glu Pro Val Trp Ser Thr Ser Gly Gln Leu Tyr Asn Pro Asp
 130 135 140
 Ala Phe Gln Phe Leu Asn Gln Ser Glu Asn Leu Asp Leu Gly Leu His
 35 145 150 155 160
 Arg Val Arg Ser Phe Arg Gln Arg Val Phe Gln Asn Gln Lys Gln Asn
 165 170 175
 Asp Phe Lys Leu Glu Gly Lys His Thr Phe Phe Ile Pro Val Asp Glu
 180 185 190
 Gly Phe Lys Pro Leu Pro Arg Pro Glu Lys Ile Asp Gln Lys
 40 195 200 205

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(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 200 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Ala	Ala	Ala	Asp	Leu	Ala	Asp	Lys	Leu	Arg	Asp	Asp	Ser	Glu	Leu	Ser
1				5					10					15	
Gln	Phe	Tyr	Ser	Leu	Leu	Glu	Ser	Asn	Gln	Ile	Ala	Asn	Ser	Thr	Leu
				20				25					30		
Ser	Leu	Arg	Ser	Cys	Thr	Ile	Phe	Val	Pro	Thr	Asn	Glu	Ala	Phe	Gln
				35				40					45		
Arg	Tyr	Lys	Ser	Lys	Thr	Ala	His	Val	Leu	Tyr	His	Ile	Thr	Thr	Glu
				50			55					60			
Ala	Tyr	Thr	Gln	Lys	Arg	Leu	Pro	Asn	Thr	Val	Ser	Ser	Asp	Met	Ala
				65			70				75			80	
Gly	Asn	Pro	Pro	Leu	Tyr	Ile	Thr	Lys	Asn	Ser	Asn	Gly	Asp	Ile	Phe
				85				90						95	
Val	Gly	Asn	Ala	Arg	Ile	Ile	Pro	Ser	Leu	Ser	Val	Glu	Thr	Asn	Ser
				100				105						110	
Asp	Gly	Lys	Arg	Gln	Ile	Met	His	Ile	Ile	Asp	Glu	Val	Leu	Glu	Pro
				115				120					125		
Leu	Thr	Val	Lys	Ala	Gly	His	Ser	Asp	Thr	Pro	Asn	Asn	Pro	Asn	Ala
				130				135					140		
Leu	Lys	Phe	Leu	Lys	Asn	Ala	Glu	Glu	Phe	Asn	Val	Asp	Asn	Ile	Gly
				145			150			155				160	
Val	Arg	Thr	Tyr	Arg	Ser	Gln	Val	Thr	Met	Ala	Lys	Lys	Glu	Ser	Val
				165				170						175	
Tyr	Asp	Ala	Ala	Gly	Gln	His	Thr	Phe	Leu	Val	Pro	Val	Asp	Glu	Gly
				180				185						190	
Phe	Lys	Leu	Ser	Ala	Arg	Ser	Ser								
				195				200							

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CLAIMS

What is claimed is:

1. A monoclonal antibody that binds to an epitope of TC1 in formalin-fixed or paraffin-embedded tissues.

5 2. A monoclonal antibody produced by the hybridoma cell line ATCC No. HB 11481, or a monoclonal antibody that binds to the same antigenic determinant as a monoclonal antibody produced by the hybridoma cell line ATCC No. HB 11481.

10 3. A method of screening for agents that inhibit expression of the TC1 gene *in vitro*, comprising

exposing a metastatic cell line in which TC1 mRNA is detectable in culture to an agent suspected of inhibiting production of said TC1 mRNA; and

15 determining the level of TC1 mRNA in said exposed cell line, wherein a decrease in the level of TC1 mRNA after exposure of said cell line to said agent is indicative of inhibition of said TC1 mRNA production.

20 4. A method of screening for agents that inhibit expression of the TC1 protein *in vitro*, comprising

exposing a metastatic cell line in which TC1 protein is detectable in culture to an agent suspected of inhibiting production of said TC1 protein; and

25 determining the level of TC1 protein in said exposed cell line, wherein a decrease in the level of TC1 protein after exposure of said cell line to said agent is indicative of inhibition of said TC1 protein production.

5. The method of claim 3, said cell line comprising JMN1B.

6. The method of claim 4, said cell line comprising JMN1B.

30 7. A method of screening for agents that inhibit expression of the TC1 gene *in vivo*, comprising

exposing a mammal having tumor cells in which TC1 mRNA is detectable to an agent suspected of inhibiting production of said TC1 mRNA; and

35 determining the level of TC1 mRNA in tumor cells of said exposed mammal, wherein a decrease in the level of TC1 mRNA after exposure of said mammal to said agent is indicative of inhibition of said TC1 mRNA production.

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8. A method of screening for agents that inhibit production of TC1 protein *in vivo*, comprising

exposing a mammal having tumor cells in which TC1 protein is detectable to an agent suspected of inhibiting production of said TC1 protein; and

determining the level of TC1 protein in tumor cells of said exposed mammal, wherein a decrease in the level of TC1 protein after exposure of said mammal to said agent is indicative of inhibition of said TC1 protein production.

9. The method of claim 7, wherein said tumor cells are breast tumor cells, colon tumor cells, or tumor cells of the gastrointestinal tract.

10. The method of claim 8, wherein said tumor cells are breast tumor cells, colon tumor cells, or tumor cells of the gastrointestinal tract.

11. A pharmaceutical composition for use in treating a late stage cancer comprising an effective amount of an inhibitor of TC1.

12. The pharmaceutical composition of claim 11 wherein said late stage cancer is one of breast cancer, colon cancer, or gastrointestinal cancer.

13. A pharmaceutical composition for use in preventing tumor cell metastasis comprising an effective amount of an inhibitor of TC1.

14. A method for detecting a tumor in a subject, comprising detecting the presence of tumor marker protein TC1 in a sample of body fluid from said subject.

15. A method for detecting a in a subject comprising the steps of:
providing a sample of body fluid from said subject;
contacting said sample with a monoclonal antibody specific for an epitope of tumor marker protein TC1; and
detecting the presence of TC1 protein in said sample, wherein the presence of TC1 protein in said sample is indicative of the presence of a tumor in said subject.

16. The method of claim 14 or 15, wherein said body fluid is selected from the group consisting of blood, urine and sputum.

17. A method for detecting a tumor in a subject, comprising detecting the presence of tumor marker protein TC1, or of mRNA encoding tumor marker protein TC1, in a sample of a tissue section from said subject.

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18. A method for detecting an invasive or metastatic tumor comprising the steps of:

providing a sample of a formalin-fixed or paraffin-embedded tissue section from said subject;

5 contacting said sample with a monoclonal antibody specific for an epitope of tumor marker protein TC1 in formalin-fixed or paraffin-embedded tissue sections; and

10 determining the level of TC1 protein in said sample, wherein the level of TC1 protein in said sample is related to the presence of an invasive or metastatic tumor in said subject.

19. The method of claim 17 or 18, wherein said tissue is breast, colon, or gastrointestinal tract tissue.

20. The method of claim 18, wherein said monoclonal antibody is a monoclonal antibody produced by the hybridoma cell line ATCC No. HB 11481.

21. The method of claim 18, wherein said monoclonal antibody is a monoclonal antibody that binds to the same antigenic determinant as a monoclonal antibody produced by the hybridoma cell line ATCC No. HB 11481.

20 22. A kit for diagnosis of an invasive or metastatic tumor in a subject, comprising
the monoclonal antibody of claim 1 or claim 2.

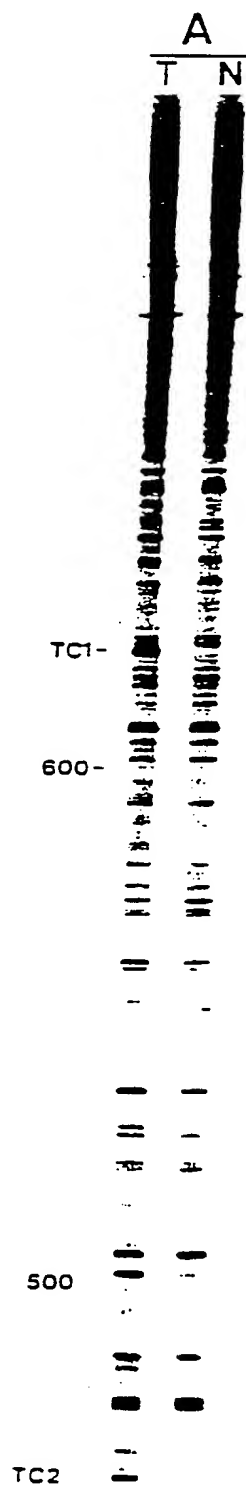
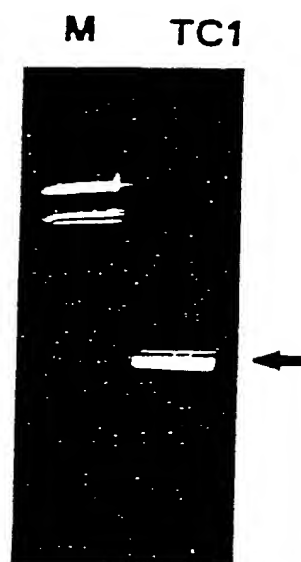


Fig. 1

A



B

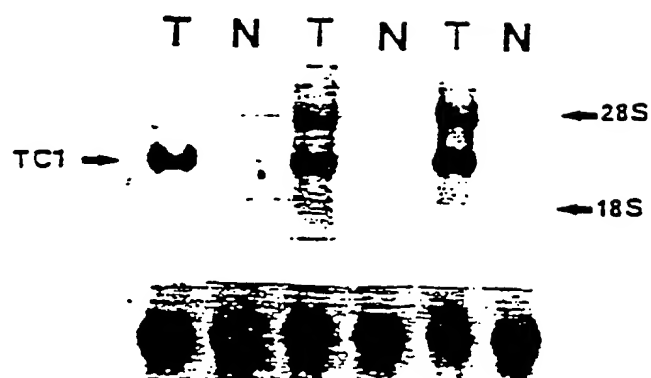


Fig. 2

1/1	31/11
CTT ATC CTT GGG AAC CAG ATT GCA ACA AAT	GGT GTT GTC CAT GTC ATT GAC CGT GTG CTT
L I H G N Q I A T N	G V V E V I D R V L
61/21	91/31
ACA CAA ATT GGT ACC TCA ATT CAA GAC TTC	ATT GAA GCA GAA GAT GAC CTT TCA TCT TTT
T Q I G T S I Q D F	I E A E D D L S S F
121/41	151/51
AGA GCA GCT GCC ATC ACA TCG GAC ATA TTG	GAG GCC CTT GGA AGA GAC GGT CAC TTC ACA
R A A A I T S D I L	E A L G R D G H F T
181/61	211/71
CTC TTT GCT CCC ACC AAT GAG GCT TTT GAG	AAA CTT CCA CGA GGT GTC CTA GAA AGG ATC
L F A P T N E A F E	R L P R G V L E R I
241/81	271/91
ATG GGA GAC AAA GTG GCT TCC GAA GCT CTT	ATG AAG TAC CAC ATC TTA AAT ACT CTC CAG
M G D K V A S E A L	M K Y H I L N T L Q
301/101	331/111
TGT TCT GAG TCT ATT ATG GGA GGA GCA GTC	TTT GAG ACC CTG GAA GGA AAT ACA ATT GAG
C S E S I M G G A V	F E T L E G N T I E
361/121	391/131
ATA GGA TGT GAC GGT GAC AGT ATA ACA GTA	AAT GGA ATC AAA ATG GTG AAC AAA AAG GAT
I G C D G D S I T V	N G I K M V N K K D
421/141	451/151
ATT GTG ACA AAT AAT GGT GTG ATC CAT TTG	ATT GAT CAG GTC CTA ATT CCT GAT TCT GCC
I V T N N G V I H L	I D Q V L I P D S A
481/161	511/171
AAA CAA GTT ATT GAG CTG GCT GGA AAA CAG	GAA ACC ACC TTC ACC GAT CTT GTG GCC CAA
K Q V I E L A G K Q	Q T T F T D L V A Q
541/181	571/191
TTA GGC TTG GCA TCT GCT CTG AGG CCA GAT	GGA GAA TAC ACT TTG CTG GCA CCT GTG AAT
L G L A S A L R P D	G E Y T L L A P V N
601/201	631/211
AAT GCA TTT TCT GAT GAT ACT CTC AGC ATG	GAT CAG
N A F S D D T L S M D Q	

Fig. 3

A



B

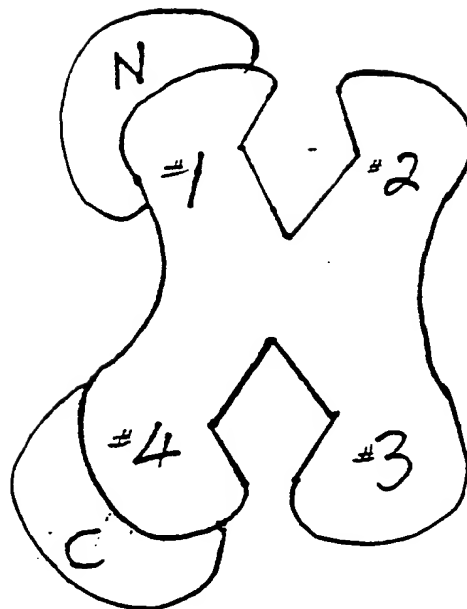


Fig. 6

homology between ... and ...

Fig. 7

MA L P A R L L A L A L A L A L P A V L L A N E A R T P Y E L
MA L T V L L A L A L A L A L G F A A L L A G P A K S P Y O L
V L Q K S S A R G G R D Q G P N V C A L C C L L G T K K K Y F S
V L Q K S S A L R G L R I O H G P N V C A V T K V I G L N R K Y F T
T K I N W Y K K S C G I O K T V L R E C C C G Y H R K E I G M K
N K I O W Y O R K C G K S I T V T S R E C C C G Y H R K V F I G D K
G C P A V L P I D H V Y I G L G I V G A T T T O R M S D A S . K
G C P A A L P I L S N L M E L G I V V G S T T Q I L M T D I R T E K
L R E E L E G I R G S F T I Y F A P S N E A W D N L D S D I R A G L
L R I E L E G I R G S F T I Y F A P S N E A W A S L P A E V L D S T
E S N V N V L L N A L E S S H M I N K R I M L T K D L K I N G M I I
V I S N V N I L L N A L R Y H M V G R I V L T D E L K E G M T L
P E H Y N N L G L F I N H Y P N G V V T V N C A R L L E G N O I
T E H Y O N S N I O I E H Y P N G V V T V N C A R L L K A D H H
A T N G V V H V E D R V L T O I G T S I G D F E A E D D S S
A T N G V V H L E D K V L T S T I T N N I O Q I T E I E D T F E T
E R A A A T S I D L E A L G R D G E F L L A E T N E A F E K
L R A A V A A S I G L N T E E G N G O V L L A E T N E A F E K
L E R G V E R I M G D I X V A S E A L M K Y E L I N T L O C I S E
I P S E T I N I R L L G D P E A L R S L L N N I R I L K S A M O A E
S I M G I A V F E T L E G N T E I I G C D G D S L V N G I K M
A I V A I L S V I E L E G T L E V G C S G D M L I N G I K A I
V N K K D I V T N G V I E L E D O V L I P D S A K I O V I E L A
I S N K D I L A T N G V I E Y E D I L L I P D S A K I L I E L A
G K Q C C . T E T I D L V A O I L G L A S A L R P D G E Y T L A P
A E S D V S T I A I E I F R I O A G L G N E I L S G S E R L L L A P
V N N A E S I D L S M D O R L L K E L L O N E I L K V X V G L
L N S V I K I N G I P P I D A E T R N I L L I R I N H I I K D C L A S
N E L S N G Q I L E I I G G K O L A V F V Y N T A V C I E N S C
K Y L M E G Q I L E I I G G K O L A V F V Y R N S C I E N S C
M E K G S K I Q I R I N G A I E I P R E I I K P A E K S L E K L K
I A A E D K I R G R Y G T L F T M D R V L T E P M G T V M D V I L K
O D K R E T T F L I L I L E A A D L K E L L T O P E D W T
G I D N R E S I M I L V A A C O S A G L T E T L N R E H V Y T
L E V P T N D A E K G M T S E I K E I L L R D K N A I L O N I I L
V E I A E T N E A E R A L P P R I E R S R L L G D A K E L A N I L K
Y H L T P G V F I G K G E E P G V T N I L K I T O G S K I F L K
Y H G D E I L V S G C I G A L V R L K I S L O G D E L . L .
E V N D T L L V N E I L K S K I E S D I M T N G V I E V V D
E V S L K I N N V V S V N I K E P V A E P T I M A T N G V I E V I T
K L E Y P . A I D T P . V G N D O L L E H L N K I K Y
N V L O I P A I N R E O E R G D E L L A D S A L E I
C I K E V R G S T E K E I P V T V Y R I P T T K V K E E G E E
. . . . E K O A L S A F S R A S O R S V
F E I E K E G T T E V I N G E S I K K Y T E C G V F V
F E L A
E E E K E T R E E E T T G F E K Y T E I S T G G E T E E
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T L K N E L C I E T T P V R I L C A N I E E E
O C K L L . E R I N

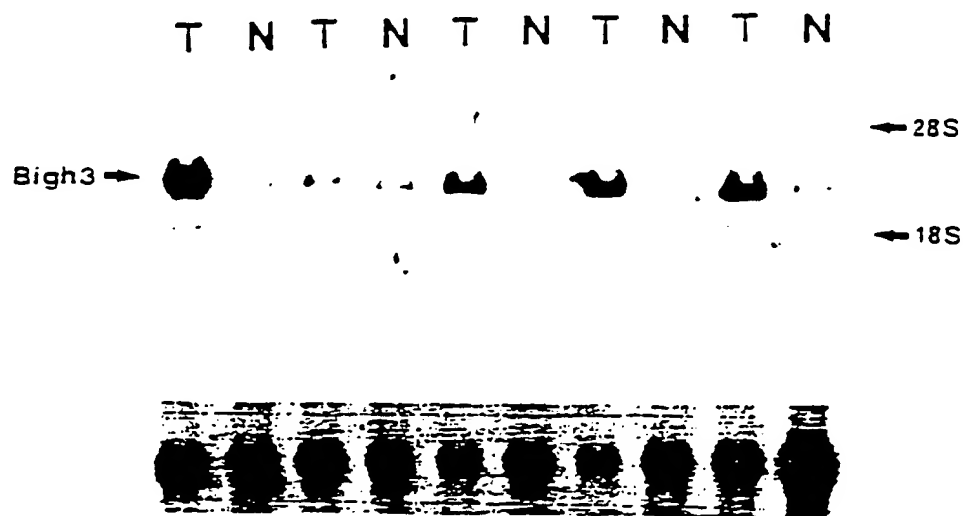


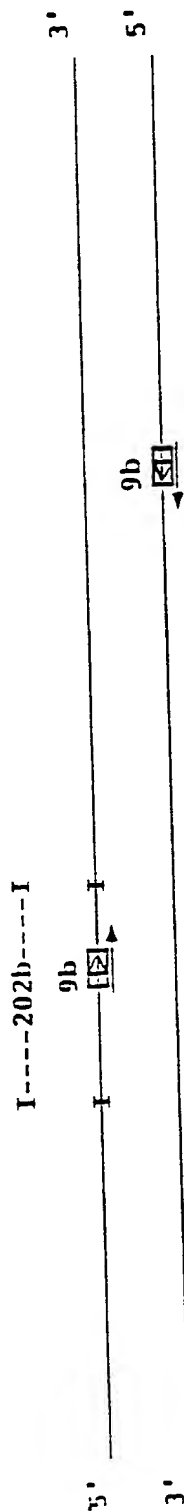
Fig. 8

Homology Between TOL and Fasciolarin I

TH	503	A	E	K	S	L	H	E	K	L	K	Q	D	K	R	F	T	T	F	L	S	L	L	E	A	A	D	L
GH	26	G	E	K	S	L	E	Y	K	I	R	D	D	P	D	L	S	Q	F	Y	S	W	L	E	H	N	E	V
DF	19	A	A	A	D	L	A	D	K	L	R	D	D	S	E	L	S	Q	F	Y	S	L	L	E	S	N	Q	I
TH		K	E	L	L	T	Q	P	G	D	W	T	L	F	V	P	T	N	D	A	F	.	.	.	K	G	M	T
GH		A	N	S	T	L	Q	L	R	Q	V	T	V	F	A	P	T	N	L	A	F	Q	N	Y	K	A	R	D
DF		A	N	S	T	L	S	L	R	S	C	T	I	F	V	P	T	N	E	A	F	Q	R	Y	K	.	.	.
TH		S	E	E	K	E	I	L	I	R	D	K	N	A	L	Q	N	I	I	L	Y	H	L	T	P	G	V	F
GH		G	D	E	N	I	I	L	Y	H	M	T	N	L	A	H	S	.	.	L	D	Q	L	G	H	K	V	L
DF		S	K	T	A	H	V	L	Y	H	I	T	T	E	A	Y	T	.	.	Q	K	R	L	P	N	T	V	S
TH		I	G	K	.	G	E	E	P	G	V	T	N	I	L	K	T	T	Q	G	.	S	K	I	F	L	K	E
GH		S	E	L	D	G	N	P	P	L	W	I	T	R	R	R	D	T	I	F	.	.	.
DF		S	D	M	A	G	N	P	P	.	.	L	Y	I	T	K	N	S	N	G	.	D	I	F	.	.	.	
TH		V	N	D	.	T	L	L	V	N	E	L	K	S	K	E	S	D	I	M	.	T	T	N	G	V	I	H
GH		V	N	N	A	R	V	L	T	.	E	R	S	N	Y	E	A	V	N	R	H	G	K	K	Q	V	L	H
DF		V	G	N	A	R	I	I	P	.	S	L	S	V	.	E	T	N	S	D	.	G	K	R	Q	I	M	H
TH		V	V	D	K	L	L	Y	P	A	D	.	T	P	.	V	G	.	.	N	D	Q	L	L	E	I	L	
GH		V	V	D	S	V	L	E	P	V	W	S	T	S	.	G	Q	L	Y	N	P	D	A	F	Q	F	L	
DF		I	H	D	E	V	L	E	P	L	.	.	T	V	K	A	G	H	S	D	T	P	N	N	P	.	.	
TH		N	K	I	I	K	Y	I	Q	I	K	F	V	R	G	S	T	F	K	E	I	P	V	T	V	Y	R	P
GH		N	Q	.	S	E	N	L	D	L	G	L	H	R	V	R	S	E	R	Q	R	.	V	F	Q	.	N	Q
DF		N	A	I	.	K	F	.	.	L	K	N	A	E	E	F	N	V	D	N	I	G	V	R	T	Y	R	S
TH		T	L	T	K	V	K	I	E	G	E	P	E	F	R	L	I	K	E	G	E	T	I	T	E	V	I	E
GH		K	Q	N	D	F	K	L	E	G	K	H	T	E	.	F	I	P	V	D	E	G	F	K	P	L	P	R
DF		Q	V	T	M	A	K	K	E	S	V	Y	D	A	A	G	Q	H	T	F	L	V	P	V	D	E	G	F
TH		G	E	E	P	E	I	K	K																			706
GH		P	E	K	I	D	Q	K																				221
DF		K	L	S	A	R	S	S																				211

Fig. 9

Fig. 10



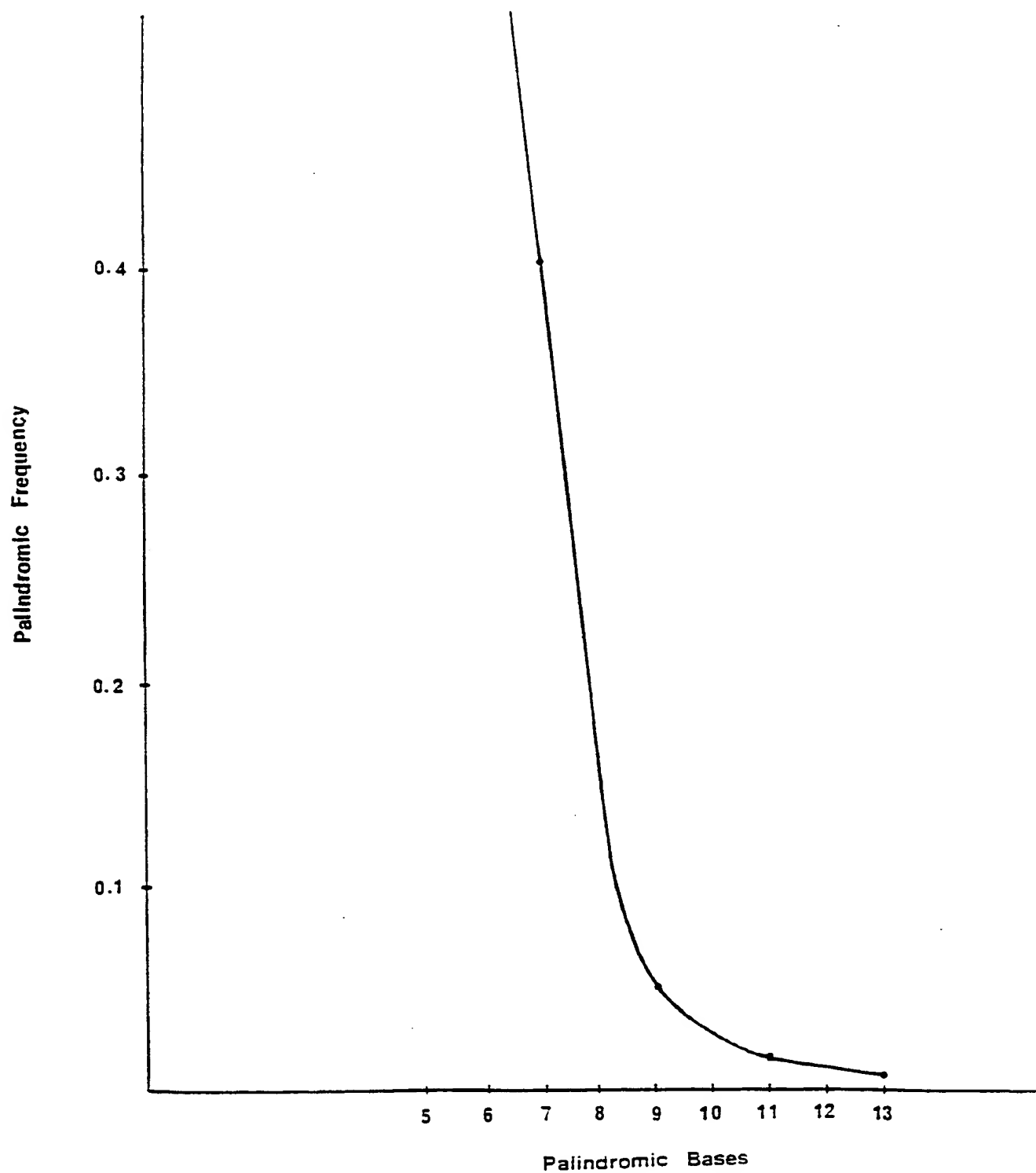


Fig. 11

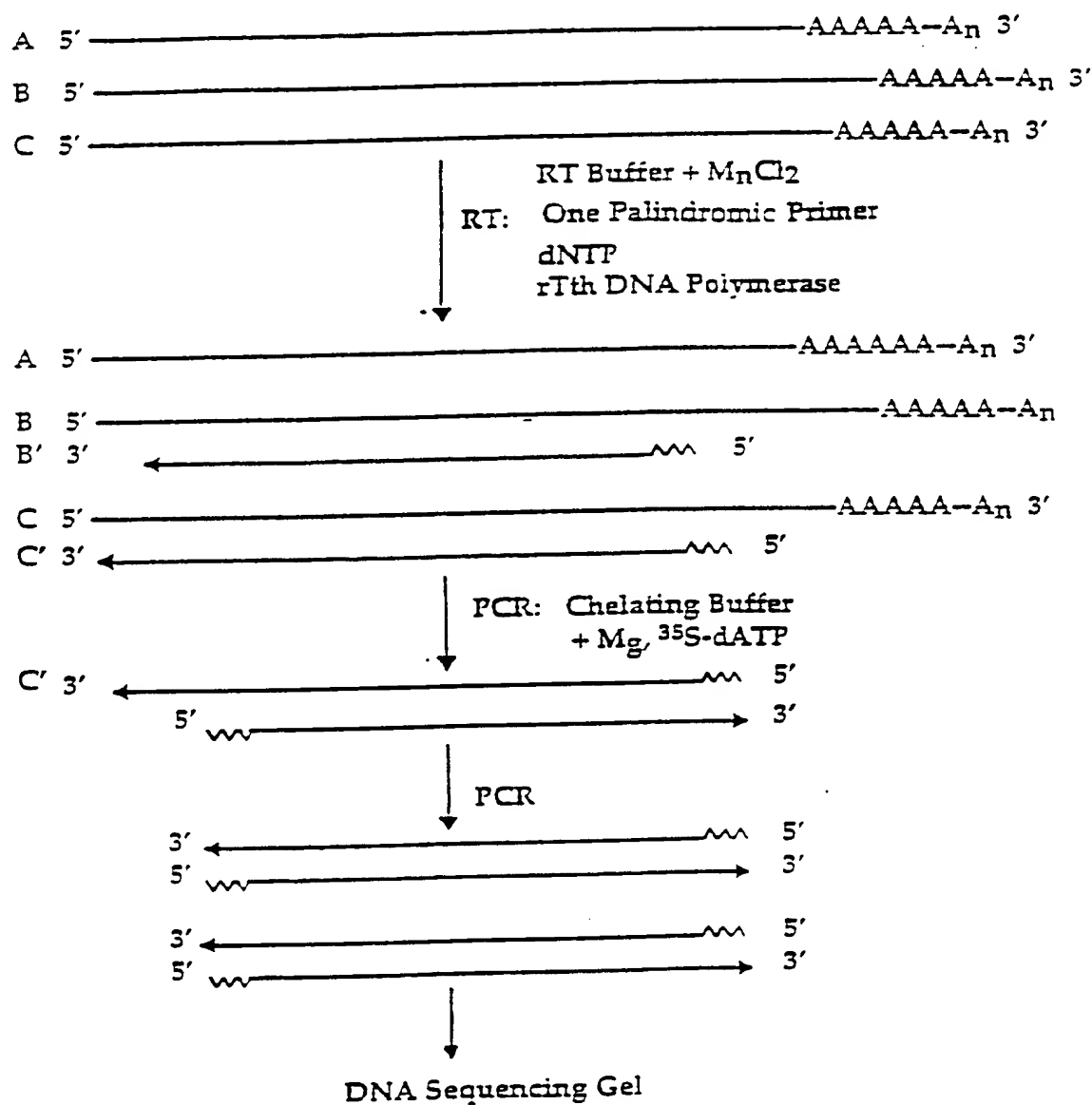


Fig. 12

Fig. 13

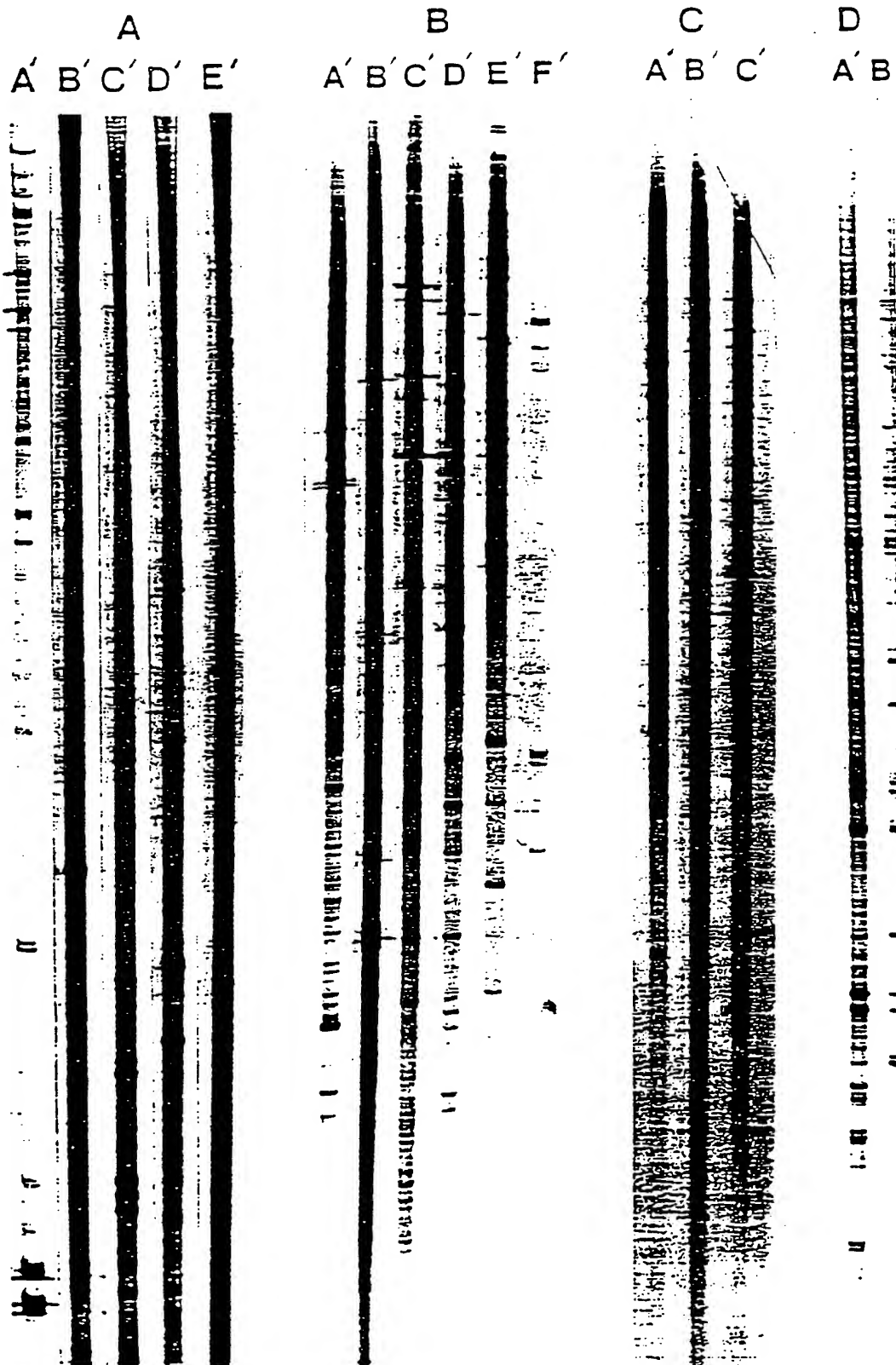


Fig. 14

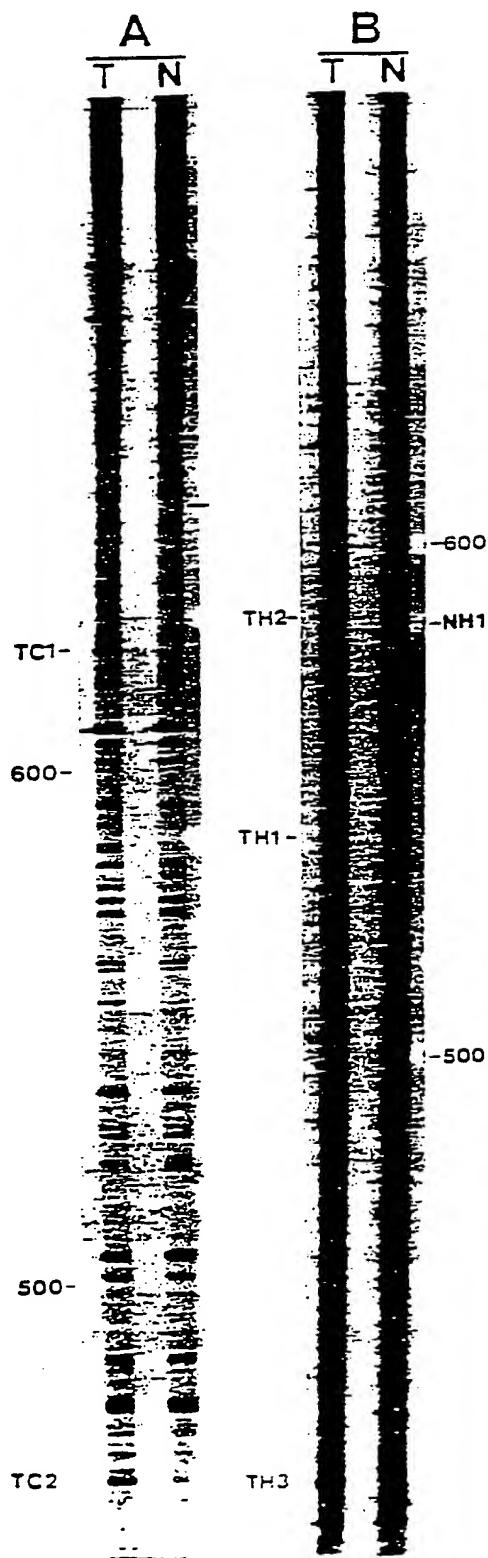




Fig. 15

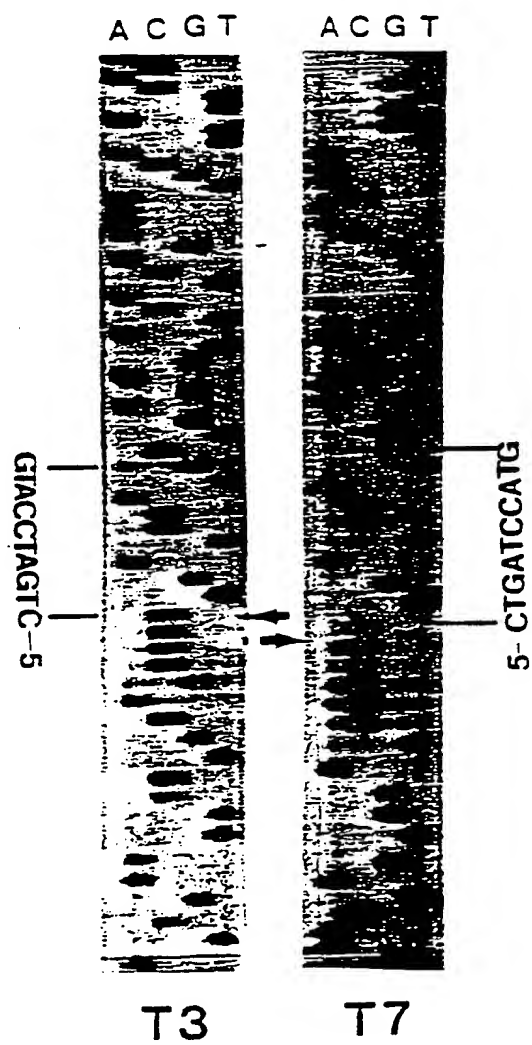
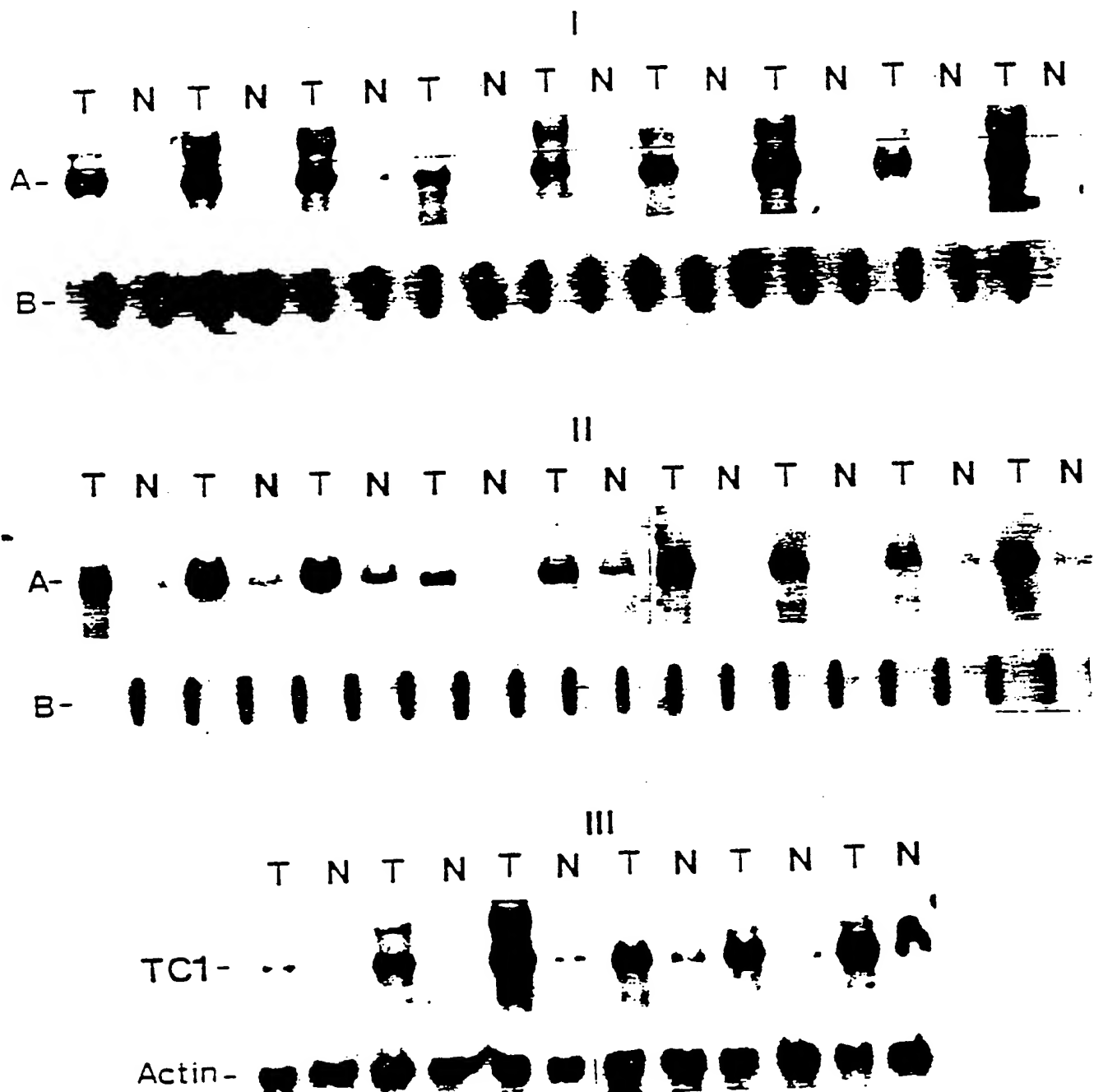


Fig. 16

Fig. 17



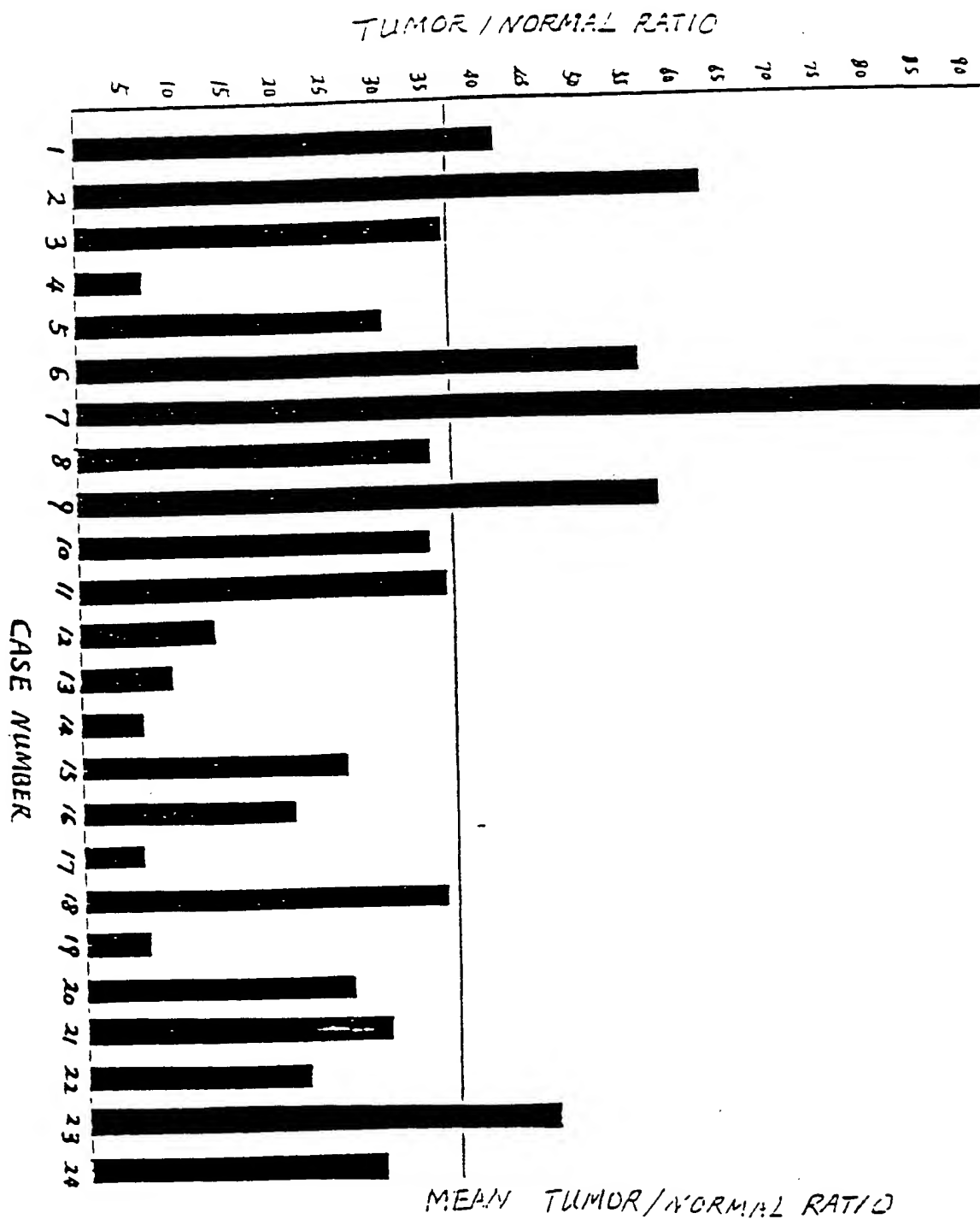


Fig. 18

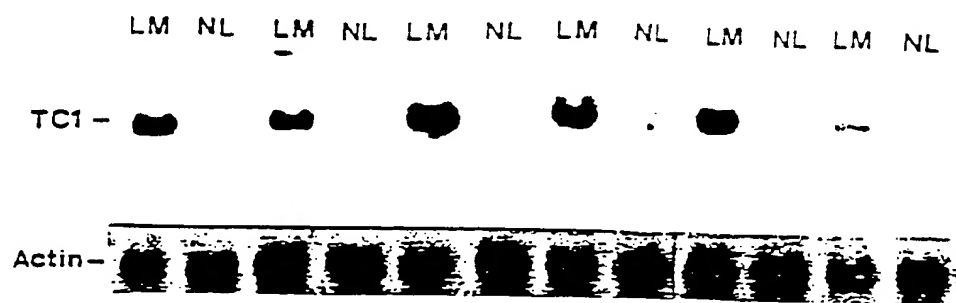
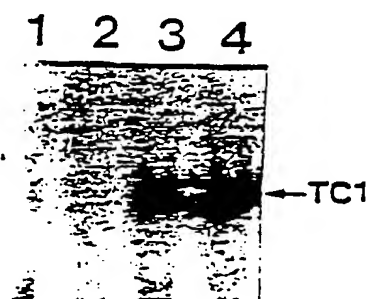


Fig. 19



1. HT29 CELL	3. HT29 TUMOR
2. CX-1 CELL	4. CX-1 TUMOR

Fig. 20

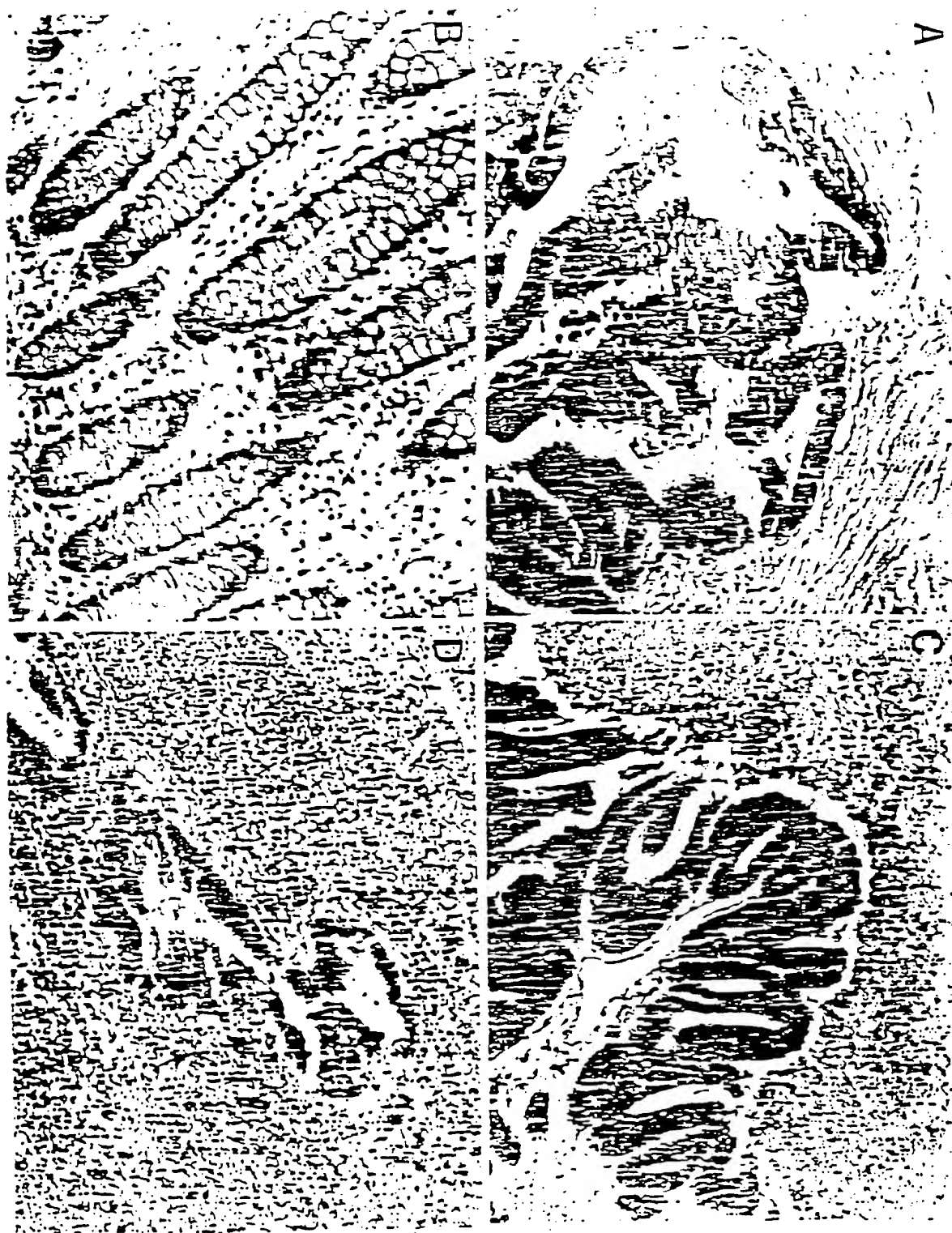


Fig. 21



Fig. 22

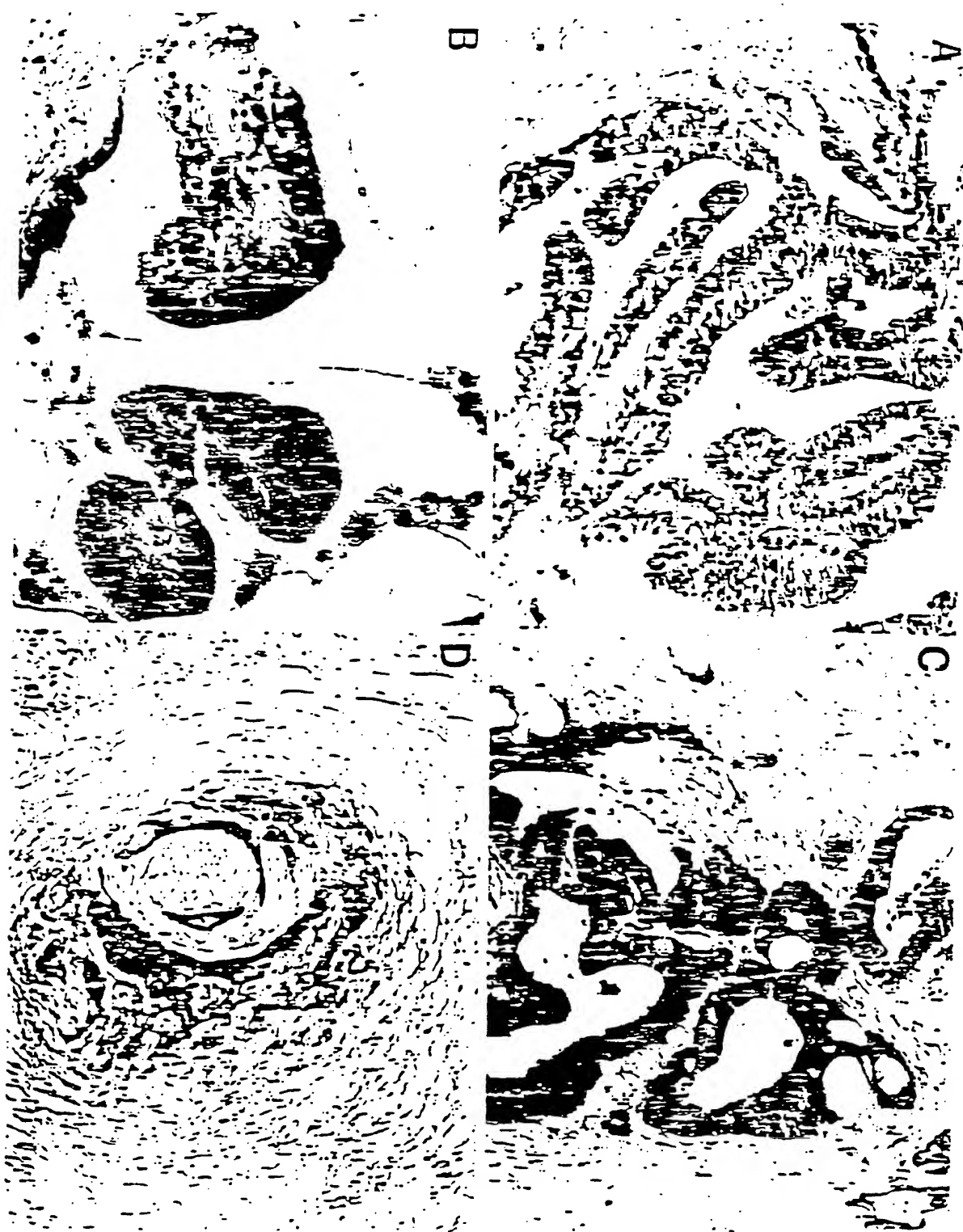


Fig. 23

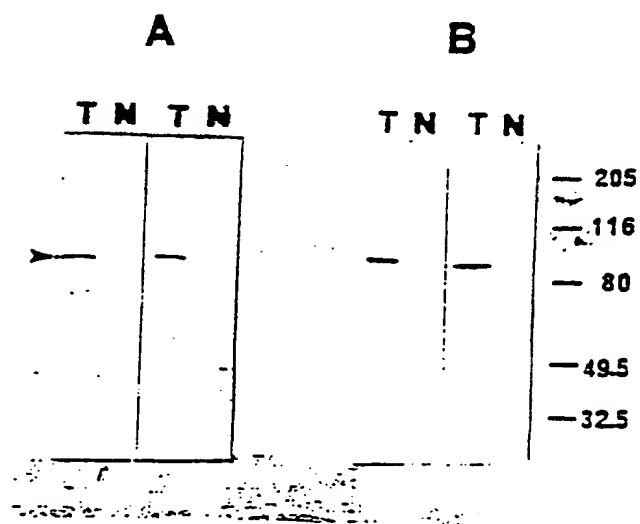
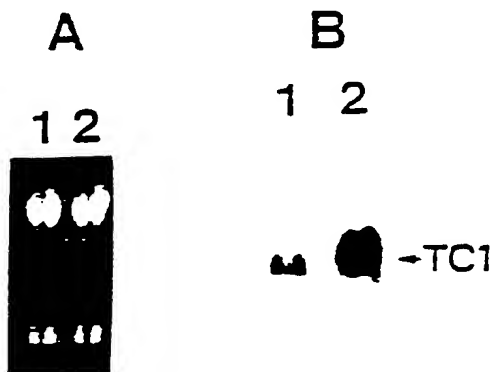


Fig. 24

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1, JM ; 2, JM1B

Fig. 25

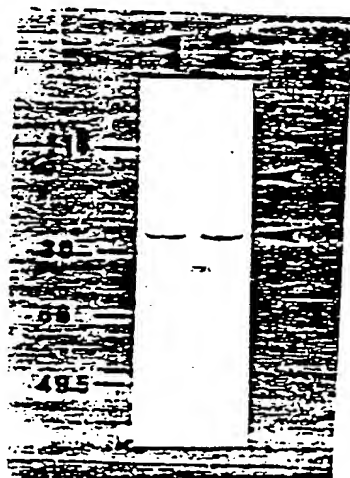


Fig. 26

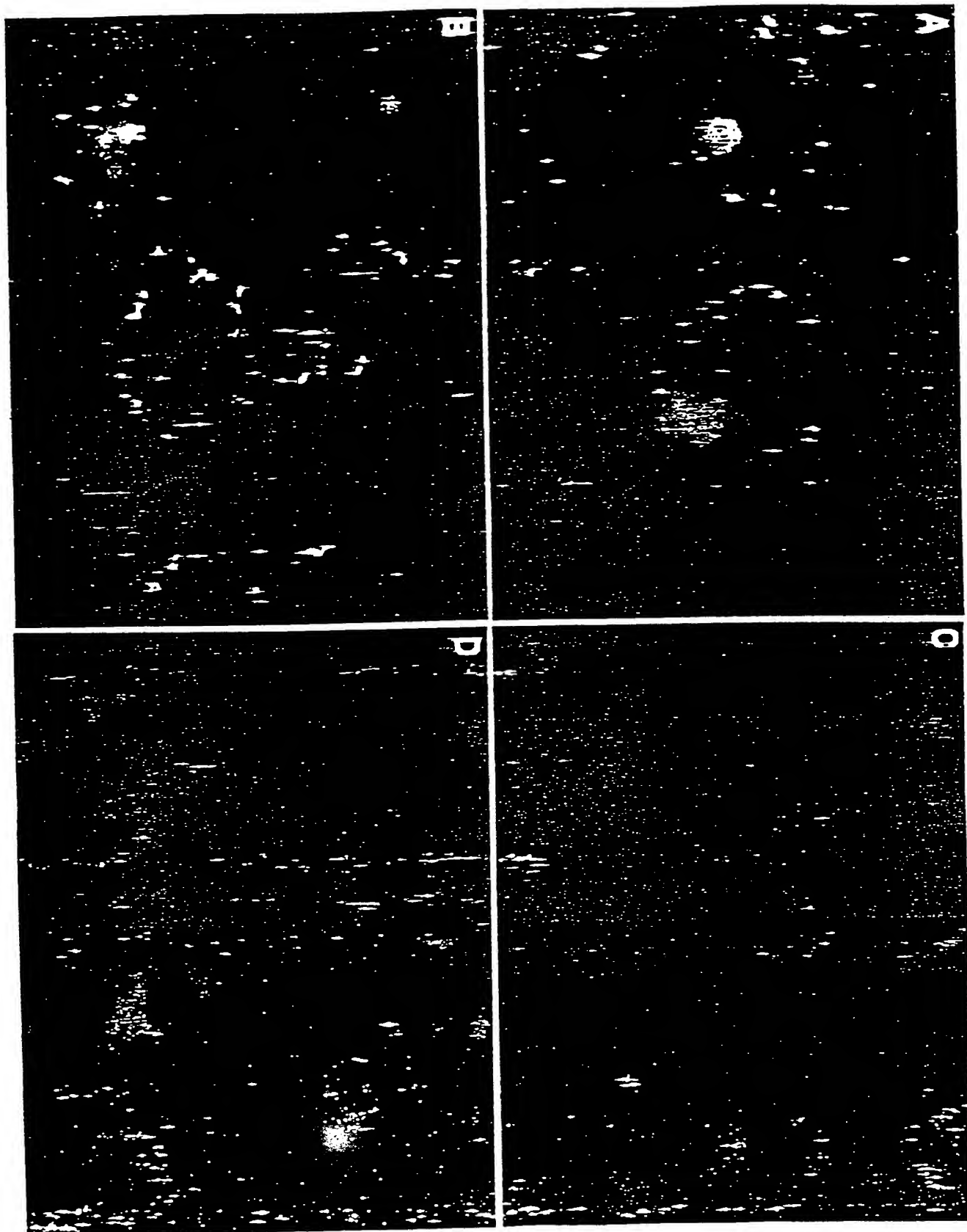


Fig. 27

Nucleotide Sequence and Deduced Amino Acid Sequence of TC1

```

1 attcgacgtctcgtccacaacagaactgcaacggagagactcaag ATG ATT CCC TTT TTA CCC ATG TTT 69
1 M I P F L P M F 8

70 TCT CTA CTA TTG CTG CTT ATT GTT AAC CCT ATA AAC GCC AAC AAT CAT TAT GAC AAG ATC 129
9 S L L L L I V N P I N A N N H Y D K I 28

130 TTG GCT CAT AGT CGT ATC AGG GGT CGG GAC CAA GGC CCA AAT GTC TGT GCC CTT CAA CAG 189
29 L A H S R I R G R D Q G P N V C A L Q Q 48

190 ATT TTG GGC ACC AAA AAG AAA TAC TTC AGC ACT TGT AAG AAC TGG TAT AAA AAG TCC ATC 249
49 I L G T K K K Y F S T C K N W Y K K S I 68

250 TGT GGA CAG AAA ACG ACT GTG TTA TAT GAA TGT TGC CCT GGT TAT ATG AGA ATG GAA GGA 309
69 C G Q K T T V L Y E C C P G Y M R M E G 88

310 ATG AAA GGC TGC CCA GCA GTT TTG CCC ATT GAC CAT GTT TAT GGC ACT CTG GGC ATC GTG 369
89 M K G C P A V L P I D H V Y G T L G I V 108

370 GGA GCC ACC ACA ACG CAG CGC TAT TCT GAC GCC TCA AAA CTG AGG GAG GAG ATC GAG GGA 429
109 G A T T Q R Y S D A S K L R E E I E G 128

430 AAG GGA TCC TTC ACT TAC TTT GCA CCG AGT AAT GAG GCT TGG GAC AAC TTG GAT TCT GAT 489
129 K G S F T Y F A P S N E A W D N L D S D 148

490 ATC CGT AGA GGT TTG GAG AGC AAC GTG AAT GTT GAA TTA CTG AAT GCT TTA CAT AGT CAC 549
149 I R R G L E S N V N V E L L N A L H S H 168

550 ATG ATT AAT AAG AGA ATG TTG ACC AAG GAC TTA AAA AAT GGC ATG ATT ATT CCT TCA ATG 609
169 M I N K R M L T K D L K N G M I I P S M 188

610 TAT AAC AAT TTG GGT CTT TTC ATT AAC CAT TAT CCT AAT GGG GTT GTC ACT GTT AAT TGT 669
189 Y N N L G L P I N H Y P N G V V T V N C 208

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Fig. 28A

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670 GCT CGA ATC ATC CAT GGG AAC CAG ATT GCA ACA AAT GGT GTT GTC CAT GTC ATT GAC CGT 729
 209 A R I I H G N Q I A T N G V V H V I D R 228
 730 GTG CTT ACA CAA ATT GGT ACC TCA ATT CAA GAC TTC ATT GAA GCA GAA GAT GAC CTT TCA 789
 229 V L T Q I G T S I Q D F I E A E D D L S 248
 790 TCT TTT AGA GCA GCT GCC ATC ACA TCG GAC ATA TTG GAG GCC CTT GGA AGA GAC GGT CAC 849
 249 S F R A A A I T S D I L E A L G R D G H 268
 850 TTC ACA CTC TTT GCT CCC ACC AAT GAG GCT TTT GAG AAA CTT CCA CGA GGT GTC CTA GAA 909
 269 F T L F A P T N E A F E K L P R G V L E 288
 910 AGG ATC ATG GGA GAC AAA GTG GCT TCC GAA GCT CTT ATG AAG TAC CAC ATC TTA AAT ACT 969
 289 R I M G D K V A S E A L M K Y H I L N T 308
 970 CTC CAG TGT TCT GAG TCT ATT ATG GGA GCA GTC TTT GAG ACG CTG GAA GGA AAT ACA 1029
 309 L Q C S E S I M G G A V F E T L E G N T 328
 1030 ATT GAG ATA GGA TGT GAC GGT GAC AGT ATA ACA GTA AAT GGA ATC AAA ATG GTG AAC AAA 1089
 329 I E I G C D G D S I T V N G I K M V N K 348
 1090 AAG GAT ATT GNG ACA AAT AAT GGT GTG ATC CAT TTG ATT GAT CAG GTC CTA ATT CCT GAT 1149
 349 K D I V T N N G V I H L I D Q V L I P D 368
 1150 TCT GCC AAA CAA GTT ATT GAG CTG GCT GGA AAA CAG CAA ACC ACC TTC ACG GAT CTT GTG 1209
 369 S A K Q V I E L A G K Q Q T T F T D L V 388
 1210 GCC CAA TTA GGC TTG GCA TCT GCT CTG AGG CCA GAT GGA GAA TAC ACT TTG CTG GCA CCT 1269
 389 A Q L G L A S A L R P D G E Y T L L A P 408
 1270 GTG AAT AAT GCA TTT TCT GAT GAT ACT CTC AGC ATG GAT CAG CGC CTC CTT AAA TTA ATT 1329
 409 V N N A P S D D T L S M D Q R L L K L I 428
 1330 CTG CAG AAT CAC ATA TTG AAA GTA AAA GTT GGC CTT AAT GAG CTT TAC AAC GGG CAA ATA 1389
 429 L Q N H I L K V K V G L N E L Y N G Q I 448

FIG. 28B

1390 CTG GAA ACC ATC GGA GGC AAA CAG CTC AGA GTC TTC GTA TAT CGT ACA GCT GTC TGC ATT 1449
 449 L E T I G G K Q L R V F V Y R T A V C I 468
 1450 GAA AAT TCA TGC ATG GAG AAA GGG AGT AAG CAA GGG AGA AAC GGT GCG ATT CAC ATA TTC 1509
 469 E N S C M E K G S K Q G R N G A I H I F 488
 1510 CGC GAG ATC ATC AAG CCA GCA GAG AAA TCC CTC CAT GAA AAG TTA AAA CAA GAT AAG CGC 1569
 489 R E I I K P A E K S L H E K L K Q D K R 508
 1570 TTT ACG ACC TTC CTC AGC CTA CTT GAA GCT GCA GAC TTG AAA GAG CTC CTG ACA CAA CCT 1629
 509 F T T F L S L L E A A D L K E L L T Q P 528
 1630 GGA GAC TGG ACA TTA TTT GTG CCA ACC AAT GAT GCT TTT AAG GGA ATG ACT AGT GAA GAA 1689
 529 G D W T L F V P T N D A F K G M T S E E 548
 1690 AAA GAA ATT CTG ATA CGG GAC AAA AAT GCT CTT CAA AAC ATC ATT CTT TAT CAC CTG ACA 1749
 549 K E I L I R D K N A L Q N I I L Y H L T 568
 1750 CCA GGA GTT TTC ATT GGA AAA GGA TTT GAA CCT GGT GTT ACT AAC ATT TTA AAG ACC ACA 1809
 569 P G V F I G K G P E P G V T N I L K T T 588
 1810 CAA GGA AGC AAA ATC TTT CTG AAA GAA GTA AAT GAT ACA CTT CTG GTG AAT GAA TTG AAA 1869
 589 Q G S K I F L L K E V N D T L L V N E L K 608
 1870 TCA AAA GAA TCT GAC ATC ATG ACA ACA AAT GGT GTA ATT CAT GTT GTA GAT AAA CTC CTC 1929
 609 S K E S D I M T T N G V I H V V D K L L 628
 1930 TAT CCA GCA GAC ACA CCT GTT GGA AAT GAT CAA CTG CTG GAA ATA CTT AAT AAA TTA ATC 1989
 629 Y P A D T P V G N D Q L L E I L N K L I 648
 1990 AAA TAC ATC CAA ATT AAG TTT GTT GGT AGC ACC TTC AAA GAA ATC CCC GTG ACT GTC 2049
 649 K Y I Q I K P V R G S T F K E I P V T V 668
 2050 TAT AGA CCC ACA CTA ACA AAA GTC AAA ATT GAA GGT GAA CCT GAA TTC AGA CTG ATT AAA 2109
 669 Y R P T L T K V K I E G E P E F R L I K 688

Fig. 28c

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2110 GAA GGT GAA ACA ATA ACT GAA GTG ATC CAT GGA GAG CCA ATT ATT AAA AAA TAC ACC AAA 2169
 689 E G E T I T E V I H G E P I I K K Y T K 708
 2170 ATC ATT GAT GGA GTG CCT GTG GAA ATA ACT GAA AAA GAG ACA CGA GAA CGA ATC ATT 2229
 709 I I D G V P V E I T E K E T R E E R I I 728
 2230 ACA GGT CCT GAA ATA AAA TAC ACT AGG ATT TCT ACT GGA GGT GGA GAA ACA GAA GAA ACT 2289
 729 T G P E I K Y T R I S T G G E T E E T 748
 2290 CTG AAG AAA TTG TTA CAA GAA GAG GTC ACC AAG GTC ACC AAA TTC ATT GAA GGT GGT GAT 2349
 749 L K K L L Q E E V T K V T K F I E G G D 768
 2350 GGT CAT TTA TTT GAA GAT GAA ATT AAA AGA CTG CTT CAG GGA GAC ACA CCC GTG AGG 2409
 769 G H L F E D E I K R L L Q G D T P V R 788
 2410 AAG TTG CAA GCC AAC AAA AAG TCA AGG ATC TAG aagacgattaaggaaggctcgttcagtgaa 2477
 789 K L Q A N K S S R I 800
 2478 aatccaaaaccagaaaaaatgtttatacaaccctaagtcaataaacctgaccttagaaaaattgtgagagccaagttgac 2557
 2558 ttcagggaactgaacatcagcacaaaagaagaatcatcaataaattctgaacacaaaatttaataatttttttctgaatg 2637
 2638 agaaacatgagggaattgtggagttagccctcctgtggtaaagggaattgaagaaaataataacaccttacaccccttttca 2717
 2718 tcttgacattaaaagtcttggttaacttttggaatccattagagagaaaaatccttgccaccagattcattacaattcaaatc 2797
 2798 gaagagttgtgaactgttatcccatgaaaagaccgagccttgatgtatgttatggatacataaaatgcacgcaagcca 2877
 2878 ttatctctccatgggaagctaagttataaaaaatagggtgcttggtgtacaaaactttttatgatcaaaaggctttgcacat 2957
 2958 ttctatatgagtggtttactggtaaatattgttttttacaactaattttgtactctcagaatgtttgtcatatgct 3037
 3038 tcttgcaatgcataatttttaactctcaaacgttttcaataaaaccatttttcagatataaaagagaattacttcaaatgag 3117
 3118 taattcagaaaaactcaagatttaagttaaaaagtggtttggacttggaataggacttttataccttcttctcgtgcc 3195

Fig. 28D

INTERNATIONAL SEARCH REPORT

Intern. Patent Application No
PCT/US 94/12502

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C07K16/30 G01N33/53 G01N33/574 C12Q1/68 A61K39/395
G01N33/577

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C07K G01N C12Q A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	EP,A,0 562 508 (HOECHST JAPAN LTD.) 29 September 1993 see tables see sequence listing ---	1-22
A	MOLECULAR BIOLOGY OF THE CELL, SUPPLEMENT, vol.4, 1993, BETHESDA MD, USA page 357A S. BAO ET AL. 'Identification and isolation of differentially expressed genes by palindromic PCR.' see abstract 2069 ---	3,7,9, 17,19
A	WO,A,93 04198 (BRITISH TECHNOLOGY GROUP LTD.) 4 March 1993 see the whole document ---	3,7,17
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Date of the actual completion of the international search

9 March 1995

Date of mailing of the international search report

20 -03- 1995

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Intern. Patent Application No
PCT/US 94/12502

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A	<p>EP,A,0 549 107 (SYNTEX (U.S.A.) INC.) 30 June 1993 see examples see figures see claims</p> <p>-----</p>	3,7,17

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/US 94/12502

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		CA-A- 2115829	04-03-93
		EP-A- 0613501	07-09-94
		GB-A- 2258867	24-02-93
		JP-T- 6510185	17-11-94
		NZ-A- 243922	26-10-94

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